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OM protein - protein search, using sw model

Run on: June 17, 2004, 11:41:01 ; Search time 70 Seconds
(without alignments)
456.112 Million cell updates/sec

Title: US-09-441-242a-2

Perfect score: 612
Sequence: 1 AECPTLGEAVTDHPDRLMAW.....VYHKIDGVEMLELLPDD 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	612	100.0	113	2	AAR94974 Human TCL
2	612	100.0	114	4	AAM80303 Human hae
3	612	100.0	114	4	AAM39823 Human pol
4	612	100.0	114	5	ABG95020 Human tra
5	612	100.0	114	5	ABG95021 Human tra
6	612	100.0	129	4	AAM41609 Human pol
7	573	93.6	113	2	AAR94975 Human TCL
8	318	52.0	76	4	AAM81164 Human hae
9	221	36.1	108	2	AAR94976 Mature T-
10	149	24.3	128	3	AAH18763 Amino aci
11	92	15.0	621	6	ABU28091 Protein e
12	91.5	15.0	625	6	ABU40542 Protein e
13	86	14.1	618	6	ABU47482 Protein e
14	86	14.1	619	6	ABU45553 Protein e
15	83	13.6	621	6	ABU15211 Protein e
16	83	13.6	621	6	ABU32391 Protein e
17	81	13.2	313	7	ADCC23769 Protein s
18	80	13.1	251	4	ABG13152 Novel hum
19	75	12.3	275	6	ABU27326 Protein e
20	74	12.1	363	3	AAH19416 A prenyl
21	74	12.1	363	3	ABB81714 Synchocy
22	74	12.1	363	5	AAU72784 Synchocy
23	73.5	12.0	802	6	AAO26991 Pseudomon
24	73.5	12.0	802	7	ADE12165 Pseudomon
25	73.5	12.0	870	6	AAO26990 Pseudomon

26	73.5	12.0	870	7	ADE12164 Pseudomon
27	73.5	12.0	874	6	AAO26989 Pseudomon
28	73.5	12.0	874	7	ADE12163 Pseudomon
29	73.5	12.0	887	6	AAO26988 Pseudomon
30	73.5	12.0	887	7	ADE12162 Pseudomon
31	73.5	12.0	900	6	AAO26987 Pseudomon
32	73.5	12.0	900	7	ADE12161 Pseudomon
33	73.5	12.0	906	6	AAO26986 Pseudomon
34	73.5	12.0	906	7	ADE12160 Pseudomon
35	73.5	12.0	931	6	AAO26985 Pseudomon
36	73.5	12.0	931	7	ADE12159 Pseudomon
37	71.5	11.7	810	4	ABG14178 Novel hum
38	70	11.4	221	5	ABG93293 C. albica
39	70	11.4	460	6	ABP70976 Epoxide h
40	69.5	11.4	115	4	ABB60092 Human tra
41	69.5	11.4	115	4	AAH94124 Human pro
42	69	11.3	520	5	ABP60956 Mus muscu
43	69	11.3	524	5	ABP60954 Mus muscu
44	69	11.3	528	5	ABP60955 Mus muscu
45	69	11.3	2944	6	ABU56436 Lung canc

ALIGNMENTS

RESULT 1
AAR94974 ID AAR94974 standard; protein, 113 AA.

AC AAR94974;

DT 23-AUG-1996 (first entry)

DE Human TCL-1 polypeptide.

KW TCL-1; chromosome-14; leukemia; lymphoma; therapy; diagnosis.

OS Homo sapiens.

XX Key Location/Qualifiers

XX Modified-site 5 /label= Phosphorylation site

XX FT /note= "casein kinase II phosphorylation site"

XX FT

XX PD 23-OCT-1995; 95WO-US013663.

XX PF 27-OCT-1994; 94US-00330272.

XX PR (UYJE-) UNIV JEFFERSON THOMAS.

XX PA (RAGG-) RAGGIO-ITALGENE SPA.

XX PI Russo G, Croce CM,

XX DR WPI; 1996-239444/24.

XX DR N-PSDB; AAT18876.

XX PT New TCL-1 protein and gene associated with chromosome 14 abnormalities -

XX PT useful to develop prode. for detection, treatment and prevention of

XX PT diseases such as T-cell leukemia(s) and lymphoma(s).

XX PS Claim 6; Page 68; 105pp; English.

XX CC The amino acid sequence of human TCL-1 protein (AAR94974) was deduced

XX CC from a cDNA clone (AAT18876) obt'd. from an ALL cell line cDNA library.

XX CC Recombinant TCL-1 can be obt'd. by incorporation of the cDNA into a vector

XX CC and expression in Escherichia coli transformants. The TCL-1 protein and

XX CC antibodies raised against it can be used for the diagnosis and treatment

XX CC of conditions associated with increased expression of TCL-1 proteins

XX CC and/or with chromosomal abnormalities, esp. T-cell leukemia and

CC lymphomas with chromosome 14 abnormalities
XX
SQ Sequence 113 AA;

Query Match 100.0%; Score 612; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 4,6e-68;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AECPTLGEAVTDHPRLMAMEKEFYVLDEKQHWLPLTTEIKRLOLRVLRRDVLGRP 60
DB 1 AECPTLGEAVTDHPRLMAMEKEFYVLDEKQHWLPLTTEIKRLOLRVLRRDVLGRP 60
QY 61 MTPPTQIGPSLLPIMWQLYPDGRYRSSDSSFWRLVYHIKIDGVEDMLLELLPDD 113
DB 61 MTPPTQIGPSLLPIMWQLYPDGRYRSSDSSFWRLVYHIKIDGVEDMLLELLPDD 113

RESULT 2

AAM80303
ID AAM80303 standard; protein; 114 AA.

AC AAM80303;

DT 13-NOV-2001 (first entry)

DE Human haematological malignancy-related antigen #1.

KW Human; cytostatic; vascular; gene therapy; vaccine; lymphoma;
KW haematological malignancy; antigen; chronic lymphocytic leukaemia;
KW follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma.

OS Homo sapiens.

PN WO200164886-A2.

XX 07-SEP-2001.

PF 01-MAR-2001; 2001WO-US007272.

PR 01-MAR-2000; 2000US-0186126P.
PR 17-MAR-2000; 2000US-0190479P.
PR 27-APR-2000; 2000US-0200545P.
PR 28-APR-2000; 2000US-0200303P.
PR 28-APR-2000; 2000US-0200779P.
PR 01-MAY-2000; 2000US-0200999P.
PR 04-MAY-2000; 2000US-0202084P.
PR 22-MAY-2000; 2000US-0206201P.
PR 14-JUL-2000; 2000US-0218950P.
PR 03-AUG-2000; 2000US-0222903P.
PR 04-AUG-2000; 2000US-0223416P.
PR 07-AUG-2000; 2000US-0223378P.

PA (CORI-) CORIXA CORP.

PI Gaiger A, Algate PA, Mannion J;

DR WPI; 2001-514842/56.

PT Compositions and methods for the detection of hematological malignancies,
PT e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and
PT Hodgkin's and T/B cell non-Hodgkin's lymphoma.

XX Claim 31; Page 504; 1252pp; English.

XX The present invention relates to compositions and methods for the
XX detection, diagnosis and therapy of haematological malignancies. The
XX present sequence is the protein sequence of a human haematological
XX malignancy related antigen. The methods of the present invention comprise
XX detecting the presence of haematological malignancy related antigen(s) in
XX a sample obtained from the patient (an increased level of the
XX polypeptide, compared to an unaffected individual, is indicative of an
XX increased risk). Haematological malignancies which can be treated using
XX the present invention are chronic lymphocytic leukaemia, lymphoma,

CC follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B
CC cell non-Hodgkin's lymphoma
XX
SQ Sequence 114 AA;

Query Match 100.0%; Score 612; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 4,7e-68;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AECPTLGEAVTDHPRLMAMEKEFYVLDEKQHWLPLTTEIKRLOLRVLRRDVLGRP 60
DB 2 AECPTLGEAVTDHPRLMAMEKEFYVLDEKQHWLPLTTEIKRLOLRVLRRDVLGRP 61
QY 61 MTPPTQIGPSLLPIMWQLYPDGRYRSSDSSFWRLVYHIKIDGVEDMLLELLPDD 113
DB 62 MTPPTQIGPSLLPIMWQLYPDGRYRSSDSSFWRLVYHIKIDGVEDMLLELLPDD 114

RESULT 3

AAM39823
ID AAM39823 standard; protein; 114 AA.

AC AAM39823;

DT 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 2968.

KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemoclastic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.

OS Homo sapiens.

PN WO200153312-A1.

XX 26-JUL-2001.

PF 26-DEC-2000; 2000WO-US034263.
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00498725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Dmanac RT;

XX WPI; 2001-442253/47.

DR N-PDB; AAI58979.

PT Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.

XX Example 4; SEQ ID NO 2968; 10078pp; English.

XX The invention relates to human nucleic acids (AA157798-AA161369) and the
XX encoded polypeptides (AAM3642-AA42213) with nootropic,
XX immunosuppressant and cytostatic activity. The polynucleotides are useful
XX in gene therapy. A composition containing a polypeptide or polynucleotide
XX system, such as peripheral nervous injuries, peripheral neuropathy and

CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokine activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification

XX Sequence 114 AA;

Query Match 100.0%; Score 612; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 4,7e-68;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AECPTLGEAVTDHPRLWAMEKFFVYLDEKQHAMLPETIEIKDRLQRLVLRREDVVLGRP 60
DB 2 AECPTLGEAVTDHPRLWAMEKFFVYLDEKQHAMLPETIEIKDRLQRLVLRREDVVLGRP 61
QY 61 MPTPTIGPSLPIPMQLYPDGGRYSSDSSFMRVLYVHIKIDGVEDMLLELPDD 113
DB 62 MPTPTIGPSLPIPMQLYPDGGRYSSDSSFMRVLYVHIKIDGVEDMLLELPDD 114

RESULT 4

ID ABG95020 standard; protein; 114 AA.

XX ABG95020;

DT 04-DEC-2002 (first entry)

DE Human translocation inv14(q11, q32) protein #1.

XX Chromosome aberration; oncogenic fusion protein; cancer;
XX proliferative disease; cellular protein isoform; heat shock protein 90;
XX HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
XX T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
XX acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
XX acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
XX papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
XX rhabdomyosarcoma; synovial sarcoma; viral infection.

OS Homo sapiens.

PN WO200269900-A2.

PD 12-SEP-2002.

PP 01-MAR-2002; 2002WO-US006518.

PR 01-MAR-2001; 2001US-0272751P.

PA (CONF-) CONFORMA THERAPEUTICS CORP.

PI Fritz LC, Burrows FJ;

XX WPI, 2002-698710/75.

DR N-PSDB; ABS73183.

PT Treating genetically-defined disease associated with chromosomal
PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
PT diseases, involves administering an inhibitor of heat shock protein 90.

PS Disclosure; Page 103; 389pp; English.

XX The invention describes a method of treating genetically-defined disease
XX associated with chromosomal aberrations yielding oncogenic fusion
XX proteins (I), treating cancerous cells containing (I) in a heterogeneous
XX cell population, treating proliferative diseases associated with mutant
XX protein or cellular protein isoforms (II), dependent on heat shock protein
XX (HSP)-90, or selectively treating cells expressing (II) involving

CC administering HSP90-inhibitor. The method is useful for treating
CC genetically-defined disease with chromosomal aberration yielding
CC oncogenic fusion protein, creating cancerous cells containing fusion
CC protein in heterogeneous cell population, treating proliferative disease
CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
CC p53), or selectively treating cells expressing mutant protein or cellular
CC protein isoform in a patient heterozygous for (II). The method is useful
CC for treating a disease e.g. haematopoietic disorder such as T or B cell
CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,
CC or a disease characterised by a solid tumour such as papillary thyroid
CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
CC synovial sarcoma. The method is also useful for treating viral
CC infections. This represents a protein encoded by the DNA sequence of a
CC chromosome aberration

XX Sequence 114 AA;

Query Match 100.0%; Score 612; DB 5; Length 114;
Best Local Similarity 100.0%; Pred. No. 4,7e-68;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AECPTLGEAVTDHPRLWAMEKFFVYLDEKQHAMLPETIEIKDRLQRLVLRREDVVLGRP 60
DB 2 AECPTLGEAVTDHPRLWAMEKFFVYLDEKQHAMLPETIEIKDRLQRLVLRREDVVLGRP 61
QY 61 MPTPTIGPSLPIPMQLYPDGGRYSSDSSFMRVLYVHIKIDGVEDMLLELPDD 113
DB 62 MPTPTIGPSLPIPMQLYPDGGRYSSDSSFMRVLYVHIKIDGVEDMLLELPDD 114

RESULT 5

ID ABG95021 standard; protein; 114 AA.

XX ABG95021;

DT 04-DEC-2002 (first entry)

DE Human translocation inv14(q11, q32) protein #2.

XX Chromosome aberration; oncogenic fusion protein; cancer;
XX proliferative disease; cellular protein isoform; heat shock protein 90;
XX HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
XX T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
XX acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
XX acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
XX papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
XX rhabdomyosarcoma; synovial sarcoma; viral infection.

OS Homo sapiens.

PN WO200269900-A2.

PD 12-SEP-2002.

PP 01-MAR-2002; 2002WO-US006518.

PR 01-MAR-2001; 2001US-0272751P.

PA (CONF-) CONFORMA THERAPEUTICS CORP.

PI Fritz LC, Burrows FJ;

XX WPI, 2002-698710/75.

DR N-PSDB; ABS73184.

PT Treating genetically-defined disease associated with chromosomal
PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
PT diseases, involves administering an inhibitor of heat shock protein 90.
XX Disclosure; Page 104; 389pp; English.

CC The invention describes a method of treating genetically-defined disease
 CC associated with chromosomal aberrations yielding oncogenic fusion
 CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
 CC cell population, treating proliferative diseases associated with mutant
 CC protein or cellular protein isoforms (II) dependent on heat shock protein
 CC (Hsp)-90, or selectively treating cells expressing (II) involving
 CC administering HSP90-inhibitor. The method is useful for treating
 CC genetically-defined disease with chromosomal aberration yielding
 CC oncogenic fusion protein, treating cancerous cells containing fusion
 CC protein in heterogeneous cell population, treating proliferative disease
 CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
 CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
 CC p53), or selectively treating cells expressing mutant protein or cellular
 CC protein isoform in a patient heterozygous for (II). The method is useful
 CC for treating a disease e.g. haematopoietic disorder such as T or B cell
 CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMM,
 CC or a disease characterised by a solid tumour such as papillary thyroid
 CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
 CC synovial sarcoma. The method is also useful for treating viral
 CC infections. This represents a protein encoded by the DNA sequence of a
 CC chromosome aberration

CC Sequence 114 AA;

Query Match 100.0%; Score 612; DB 5; Length 114;
 Best Local Similarity 100.0%; Pred. No. 4.7e-68;
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AECPTLGEAVTDHPRLMAWEKFFVYLDKQHAMLPITIEIKDRLQRLVLRREDVYLGRP 60

DB 2 AECPTLGEAVTDHPRLMAWEKFFVYLDKQHAMLPITIEIKDRLQRLVLRREDVYLGRP 61

QY 61 MTPFOIGPSLLPIMQOLYPDGRYSSDSSFWRLVYHIKIDGVEDMLLELPDD 113

DB 62 MTPFOIGPSLLPIMQOLYPDGRYSSDSSFWRLVYHIKIDGVEDMLLELPDD 114

RESULT 6
 AAM41609
 ID AAM41609 standard; protein; 129 AA.

AC AAM41609;

DT 22-OCT-2001 (first entry)

XX Human polypeptide SEQ ID NO 6540.

XX Human, noctropic, immunosuppressant, cytosolic; gene therapy; cancer;
 XX peripheral nervous system; neuropathy; central nervous system; CNS;
 XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 XX chemokine; thrombolytic; drug screening; arthritis; inflammation;
 XX leukaemia.

XX Homo sapiens.

OS WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US034263.

XX 23-DEC-1999; 99US-00471275.

XX 21-JAN-2000; 2000US-0048725.

XX 25-APR-2000; 2000US-0052317.

XX 20-JUN-2000; 2000US-00598042.

XX 19-JUL-2000; 2000US-00620312.

XX 03-AUG-2000; 2000US-00653450.

XX 14-SEP-2000; 2000US-00662191.

XX 19-OCT-2000; 2000US-00693036.

XX 29-NOV-2000; 2000US-00727344.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Aundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA,
 PI Zhou P, Goodrich R, Drmanac RT;
 XX WPI; 2001-442253/47.

DR N-PSDB; AAI60765.

PT Novel nucleic acids and polypeptides, useful for treating disorders such

XX as central nervous system injuries.

XX Example 2; SEQ ID NO 6540; 10078pp; English.

CC The invention relates to human nucleic acids (AA157798-AA161369) and the
 CC encoded polypeptides (AAM38642-AA42213) with noctropic,
 CC immunosuppressant and cytosolic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders. Note: The sequence data for this patent did not form
 CC part of the printed specification

XX Sequence 129 AA;

Query Match 100.0%; Score 612; DB 4; Length 129;
 Best Local Similarity 100.0%; Pred. No. 5.5e-68;
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AECPTLGEAVTDHPRLMAWEKFFVYLDKQHAMLPITIEIKDRLQRLVLRREDVYLGRP 60

DB 17 AECPTLGEAVTDHPRLMAWEKFFVYLDKQHAMLPITIEIKDRLQRLVLRREDVYLGRP 76

QY 61 MTPFOIGPSLLPIMQOLYPDGRYSSDSSFWRLVYHIKIDGVEDMLLELPDD 113

DB 77 MTPFOIGPSLLPIMQOLYPDGRYSSDSSFWRLVYHIKIDGVEDMLLELPDD 129

RESULT 7

AAAR94975
 ID AAR94975 standard; protein; 113 AA.

AC AAR94975;

DT 23-AUG-1996 (first entry)

XX Human TCL-1 polypeptide.

XX TCL-1; chromosome-14; leukaemia; lymphoma; therapy.

XX Homo sapiens.

OS Location/Qualifiers

XX Key MISC-difference 31 /note= "unidentified amino acid"

XX MISC-difference 46 /note= "unidentified amino acid"

XX MISC-difference 47 /note= "unidentified amino acid"

XX MISC-difference 55 /note= "unidentified amino acid"

XX WO9613514-A1.

XX 09-MAY-1996.

XX 23-OCT-1995; 95WO-US013663.

XX 27-OCT-1994; 94US-00330272.
 PR (UYJE-) UNIV JEFFERSON THOMAS.
 PA (RAGG-) RAGGIO-ITALGENE SPA.
 PA
 XX
 PI Russo G, Croce CM;
 XX
 DR WPI; 1996-239444/24.
 DR N-PSDB; AAT18877.
 XX
 PT New TCR-1 protein and gene associated with chromosome 14 abnormalities -
 PT useful to develop prods. for detection, treatment and prevention of
 PT diseases such as T-cell leukaemia(s) and lymphoma(s).
 XX
 PS Disclosure; Page 69-72; 105pp; English.
 CC
 CC The amino acid sequence (AAR94975) of human TCR-1 protein was deduced
 CC from the exon sequences of the TCR-1 gene (AAT18877). A sequence deduced
 CC from a cDNA clone is given in AAR94974. The TCR-1 gene is expressed at
 CC high levels in leukaemic cells carrying a t(14;14)(q11;q32) translocation
 CC or an inv(14)(q11;q32) inversion. The TCR-1 protein, and antibodies
 CC raised against it, can be used for the diagnosis or treatment of
 CC conditions associated with increased expression of TCR-1 proteins and/or
 CC with chromosome 14 abnormalities, esp. T-cell leukaemia and lymphoma
 XX
 SQ Sequence 113 AA;

Query Match 93.6%; Score 573; DB 2; Length 113;
 Best Local Similarity 95.6%; Pred. No. 3.4e-63;
 Matches 108; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AECPTLGEAVTDPRLMAWEKRYVLDKQHAWLPITTEIKRQLRLVLRREDVVLGR 60
 |||||
 DB 1 AECPTLGEAVTDPRLMAWEKRYVLDKQKXCLPITTEIKRQLRXVLRREDVVLGR 60
 |||||
 QY 61 MPTPIGSLPLIMQVLPDGRYSSDSFMRVYHIKIDGVEDMLLELPDD 113
 |||||
 DB 61 MPTPIGSLPLIMQVLPDGRYSSDSFMRVYHIKIDGVEDMLLELPDD 113
 |||||

RESULT 8
 AAM81164
 ID AAM81164 standard; protein; 76 AA.
 AC AAM81164;
 XX
 DT 13-NOV-2001 (first entry)
 DE Human haematological malignancy-related antigen #862.
 XX
 KW Human; cytostatic; vascular; gene therapy; vaccine; lymphoma;
 KW haematological malignancy; antigen; chronic lymphocytic leukaemia;
 KW follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma.
 XX
 OS Homo sapiens.
 XX
 FN WO200164886-A2.
 XX
 PD 07-SEP-2001.
 XX
 PF 01-MAR-2001; 2001WO-US007272.
 XX
 PR 01-MAR-2000; 2000US-0186126P.
 PR 17-MAR-2000; 2000US-0190479P.
 PR 27-APR-2000; 2000US-0200545P.
 PR 28-APR-2000; 2000US-0200303P.
 PR 28-APR-2000; 2000US-0200779P.
 PR 01-MAY-2000; 2000US-0200999P.
 PR 04-MAY-2000; 2000US-0202084P.
 PR 22-MAY-2000; 2000US-0206201P.
 PR 14-JUL-2000; 2000US-0218950P.
 PR 03-AUG-2000; 2000US-0222903P.

PR 04-AUG-2000; 2000US-0223416P.
 PR 07-AUG-2000; 2000US-0223378P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Galger A, Algate PA, Mannion J;
 XX
 DR WPI; 2001-514842/56.
 XX
 PT Compositions and methods for the detection of hematological malignancies,
 PT e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and
 PT Hodgkin's and T/B cell non-Hodgkin's lymphoma.
 XX
 PS Claim 1; Page 859; 1252pp; English.

CC The present invention relates to compositions and methods for the
 CC detection, diagnosis and therapy of haematological malignancies. The
 CC present sequence is the protein sequence of a human haematological
 CC malignancy related antigen. The methods of the present invention comprise
 CC detecting the presence of haematological malignancy related antigen(s) in
 CC a sample obtained from the patient (an increased level of the
 CC polypeptide, compared to an unaffected individual, is indicative of an
 CC increased risk). Haematological malignancies which can be treated using
 CC the present invention are chronic lymphocytic leukaemia, lymphoma,
 CC follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B
 CC cell non-Hodgkin's lymphoma
 XX
 SQ Sequence 76 AA;

Query Match 52.0%; Score 318; DB 4; Length 76;
 Best Local Similarity 100.0%; Pred. No. 1.2e-31;
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AECPTLGEAVTDPRLMAWEKRYVLDKQHAWLPITTEIKRQLRLVLRREDVVLGR 59
 |||||
 DB 18 AECPTLGEAVTDPRLMAWEKRYVLDKQHAWLPITTEIKRQLRLVLRREDVVLGR 76
 |||||

RESULT 9
 AAR94976
 ID AAR94976 standard; protein; 108 AA.
 AC AAR94976;
 XX
 DT 23-AUG-1996 (first entry)
 DE Mature T-cell proliferative 1 protein.
 XX
 KW TCR-1; chromosome-14; leukaemia; lymphoma; therapy; diagnosis;
 KW T-cell proliferative 1 protein.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 108
 FT /note= "unidentified amino acid"
 XX
 FN WO9613514-A1.
 XX
 PD 09-MAY-1996.
 XX
 PF 23-OCT-1995; 95WO-US013663.
 XX
 PR 27-OCT-1994; 94US-00330272.
 XX
 PA (UYJE-) UNIV JEFFERSON THOMAS.
 PA (RAGG-) RAGGIO-ITALGENE SPA.
 XX
 PI Russo G, Croce CM;
 XX
 DR WPI; 1996-239444/24.
 XX
 PT New TCR-1 protein and gene associated with chromosome 14 abnormalities -

PT useful to develop prods. for detection, treatment and prevention of
PT diseases such as T-cell leukaemia(s) and lymphoma(s).
XX
PS Disclosure; Page 69; 105pp; English.
XX
CC The mature T-cell proliferative 1 protein (AAR94976) is involved in a
CC translocation of chromosome 14 and X chromosome t(14;X)(q11;q28). It
CC shows 40% amino acid sequence homology to human Tc1-1 protein (AAR94974),
CC which is associated with chromosome 14 abnormalities leading to leukaemia
CC and lymphoma
XX
SQ Sequence 108 AA;
Query Match 36.1%; Score 221; DB 2; Length 108;
Best Local Similarity 40.2%; Pred. No. 2.4e-19;
Matches 43; Conservative 23; Mismatches 39; Indels 2; Gaps 1;
QY 7 GEAVTDHEDRLAMEKPYLDEKOHAWLPLTIEIKDRLQLRREDDVVLGRPMTPTQI 66
DB 3 GEDVGAPDPDHLMWQEGYRDEYQRTWVAVVEEESFLARAV--QGIQVPLGDAPPSHL 60
QY 67 GPSLLPTMWQLYPDGRYSSDSFWRLVYHIKIDGVEDMLLELPDD 113
DB 61 LTSQLPLMWQLYPERRYMNNRSLMQLIOHMLMVGVELLKLPLDD 107
RESULT 10
AAB18763
ID AAB18763 standard; protein; 128 AA.
XX
AC AAB18763;
XX
DT 22-JAN-2001 (first entry)
XX
DE Amino acid sequence of the human Tc1-1b protein.
XX
XX Tc1-1; Tc1-1b; T cell malignancy; chromosome 14 abnormality; lymphoma;
KM T-cell leukaemia; immunodeficiency syndrome; ataxia-telangiectasia.
XX
OS Homo sapiens.
XX
PN W020055169-A1.
XX
PD 21-SEP-2000.
XX
PF 15-MAR-2000; 2000MO-US006612.
XX
PR 15-MAR-1999; 99US-0124714P.
XX
PA (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI Croce CM, Pekarsky Y;
XX
DR WPI; 2000-611514/58.
DR N-PSDB; AAA75822.
XX
PT Novel nucleic acid of Tc1-1 gene family, Tc1-1b, expressed in low levels
PT in normal bone marrow and peripheral lymphocytes, but activated in T-cell
PT leukemia and lymphoma, used to identify chromosome 14 abnormalities.
XX
PS Claim 7; Page 64; 70pp; English.
XX
CC The present sequence represents a human Tc1-1b protein. The Tc1-1b gene
CC is implicated in the development of T cell malignancies. Fragments of Tc1-
CC 1b cDNA sequences are used for detecting a target sequence indicating a
CC chromosome 14 abnormality, such as a (14;14)(q11;q32) translocation or a
CC (14)(q11;q32) inversion. Tc1-1b antisense sequences and antibodies are
CC useful for treating a disease state such as T-cell leukemia or lymphoma
CC associated with a chromosome 14 abnormality. The Tc1-1b gene and its gene
CC product are useful for treating disease states associated with the Tc1-1b
CC locus on chromosome protein including T-prolymphocytic leukaemias, acute
CC and chronic leukaemias associated with the immunodeficiency syndrome
CC ataxia-telangiectasia (AT)

XX
SQ Sequence 128 AA;
Query Match 24.3%; Score 149; DB 3; Length 128;
Best Local Similarity 29.2%; Pred. No. 2.8e-10;
Matches 33; Conservative 21; Mismatches 45; Indels 14; Gaps 1;
QY 14 PDRLMAWEKPYLDEKOHAWLPLTIEIKDRLQ-----LRVLLREDDVVLGR 59
DB 13 PGRIMTRPGIYLPDEERTWTVVVRNPSRRREKAPASQGSRYEPSTITVLMQAAVHTRE 72
QY 60 PMTPYQIGPSLLPTMWQLYPDGRYSSDSFWRLVYHIKIDGVEDMLLELPDD 112
DB 73 LLSGQWPFQSLPAVWQLYGRKYRADSSFWELIADHGQIDSEQLVLTGQPE 125
RESULT 11
ABU28091
ID ABU28091 standard; protein; 621 AA.
XX
AC ABU28091;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #13618.
XX
KM Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Enterobacter cloacae.
XX
PN W020027183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002MO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
XX
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342933P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haeselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick UD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-023926/02.
DR N-PSDB; ACA31961.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 56015; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 613 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a

CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
CC
XX
SQ Sequence 621 AA;

Query Match 15.0%; Score 92; DB 6; Length 621;
Best Local Similarity 33.3%; Pred. No. 0.026;
Matches 25; Conservative 16; Mismatches 26; Indels 8; Gaps 3;

OY 16 RLMAWEKRV---YLDKQHWLPLRT--EIKDRLQLRLVLRREDVVLGRMPTQTGP 68
DB 440 KTWAMETALIQIREVSETEYAVPIRTGHPGEVRL-IDVLRLPEVLVFEPLMTVTPGNK 498
OY 69 SLPLIMQVLPDGRY 83
DB 499 ALPLVLMQLPFPNRY 513

RESULT 12

ABU40542
ID ABU40542 standard; protein; 625 AA.

AC ABU40542;

DT 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #26069.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

OS Proteus sp.

XX WO200277183-A2.

PD 03-OCT-2002.

PF 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

DR N-PSDB; ACA44412.

XX New antisense nucleic acids, useful for identifying proteins or screening

CC for homologous nucleic acids required for cellular proliferation to

CC isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 68466; 1766pp; English.

CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
CC
XX
SQ Sequence 625 AA;

Query Match 15.0%; Score 91.5; DB 6; Length 625;
Best Local Similarity 33.3%; Pred. No. 0.03;
Matches 26; Conservative 13; Mismatches 24; Indels 15; Gaps 4;

OY 16 RLMAWEKRVYLDKQHWLPLRT--EIKDRLQLRLVLRREDVVLGRMPTQTGP 65
DB 441 KTWAME--TALDQRESEQSLPIRTGDPAGEVR--LVDVLRLPEVLVFEPLMTLIP 495
OY 66 IGPLSLIMQVLPDGRY 83
DB 496 SNKAILPLIMQLPFPNRY 513

RESULT 13

ABU47482
ID ABU47482 standard; protein; 618 AA.

AC ABU47482;

DT 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #33009.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

OS *Salmonella typhi*.

XX WO200277183-A2.

PD 03-OCT-2002.

PF 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

ABU15211	ABU15211 standard; protein; 619 AA.
ID	ABU15211 standard; protein; 619 AA.
XX	
AC	ABU15211;
XX	
DT	19-JUN-2003 (first entry)
XX	
DE	Protein encoded by prokaryotic essential gene #738.
XX	
KM	Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX	
OS	<i>Escherichia coli</i> .
XX	
XX	
PD	MO200277183-A2.
XX	
PD	03-OCT-2002.
XX	
PF	21-MAR-2002; 2002MO-US009107.
XX	
PR	21-MAR-2001; 2001US-00815242.
PR	06-SEP-2001; 2001US-00948993.
PR	25-OCT-2001; 2001US-0342923P.
PR	08-FEB-2002; 2002US-00072851.
PR	06-MAR-2002; 2002US-0362699P.
XX	
PA	(ELIT-) ELITRA PHARM INC.
XX	
PI	Wang L, Zamudio C, Malone C, Hasselbeck R, Ohlsen KL, Zyskind JW,
PI	Wall D, Traxwick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH,
XX	
XX	WPI; 2003-029926/02.
DR	N-PSDB; ACA19081.
XX	
PT	New antisense nucleic acids, useful for identifying proteins or screening
PT	for homologous nucleic acids required for cellular proliferation to
PT	isolate candidate molecules for rational drug discovery programs.
XX	
PS	Claim 25; SEQ ID NO 43135; 1766bp; English.
XX	
CC	The invention relates to an isolated nucleic acid comprising any one of
CC	the 6213 antisense sequences given in the specification where expression
CC	of the nucleic acid inhibits proliferation of a cell. Also included are:
CC	(1) a vector comprising a promoter operably linked to the nucleic acid
CC	encoding a polypeptide whose expression is inhibited by the antisense
CC	nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC	polypeptide or its fragment whose expression is inhibited by the
CC	antisense nucleic acid; (4) an antibody capable of specifically binding
CC	the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC	proliferation or the activity of a gene in an operon required for
CC	proliferation; (7) identifying a compound that influences the activity of
CC	the gene product or that has an activity against a biological pathway
CC	required for proliferation, or that inhibits cellular proliferation; (8)
CC	identifying a gene required for cellular proliferation or the biological
CC	pathway in which a proliferation-regulated gene or its gene product lies
CC	or a gene on which the best compound that inhibits proliferation of an
CC	organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC	compound's activity; (11) a culture comprising strains in which the gene
CC	product is overexpressed or underexpressed; (12) determining the extent
CC	to which each of the strains is present in a culture or collection of
CC	strains; or (13) identifying the target of a compound that inhibits the
CC	proliferation of an organism. The antisense nucleic acids are useful for
CC	identifying proteins or screening for homologous nucleic acids required
CC	for cellular proliferation to isolate candidate molecules for rational
CC	drug discovery programs, or for screening homologous nucleic acids
CC	required for proliferation in cells other than <i>S. aureus</i> , <i>S. typhimurium</i> ,
CC	<i>K. pneumoniae</i> or <i>P. aeruginosa</i> . The present sequence is encoded by one of
CC	the target prokaryotic essential genes. Note: The sequence data for this
CC	patent did not form part of the printed specification, but was obtained
CC	in electronic format directly from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences
XX	
XX	Sequence 619 AA;
XX	

	Query March	13.6%	Score 83;	DB 6;	Length 619;
Oy	Best Local Similarity	28.4%;	Pred. No. 0.34;		
Dd	Matches 21; Conservative	21;	Mismatches 26;	Indels 6;	Gaps 3;
	16 RUMAME-----KFVYLDEKOHAMLP-TEIHDRLOQLRLRREDYVLGRPM-TPNQIGSPS	69			
	: :: :: :: :: :: :: :: :: :: :: :	:			
Dd	440 KTWMEHFAFDIREVSDFEAFAPVRITGHPDNEVKLIDLVLRPEVLFEEPLWTVIPGNKA	499			
Oy	70 LPIIMMOLYPDGRY	83			
	::: :: :: :: :	:			
Dd	500 ILPILMSLEFPHHRY	513			

Search completed: June 17, 2004, 14:26:21
Job time : 72 secs

SQ Sequence 619 AA;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 17, 2004, 14:26:27 ; Search time 503 Seconds
(without alignments)
63.422 Million cell updates/sec

Title: US-09-441-242a-2

Perfect score: 612

Sequence: 1 AECPTLGEAVTDHPRLMW.....VYHIKIDGVEDMLLELPDD 113

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: Published Applications_AA:*
2: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	612	100.0	114	9	US-09-796-692-666
2	612	100.0	114	14	US-10-040-862-666
3	612	100.0	114	15	US-10-057-475B-666
4	612	100.0	114	15	US-10-154-884B-666
5	612	100.0	121	15	US-10-057-475B-10485
6	612	100.0	121	15	US-10-154-884B-10485
7	318	52.0	76	9	US-09-796-692-1528
8	318	52.0	76	14	US-10-040-862-1528
9	318	52.0	76	15	US-10-057-475B-1528
10	318	52.0	76	15	US-10-154-884B-1528
11	92	15.0	621	12	US-10-282-122A-56015
12	91.5	15.0	623	12	US-10-282-122A-56015
13	86	14.1	618	12	US-10-282-122A-68466
14	86	14.1	619	12	US-10-282-122A-75406
15	83	13.6	619	12	US-10-282-122A-73477
					Sequence 43135, A

16	83	13.6	621	12	US-10-282-122A-60315	Sequence 60315, A
17	81	13.2	313	12	US-10-440-503-36	Sequence 36, Appl
18	81	13.2	313	12	US-10-461-925-36	Sequence 36, Appl
19	81	13.2	313	14	US-10-146-772-36	Sequence 36, Appl
20	81	13.2	313	15	US-10-241-742-36	Sequence 36, Appl
21	81	13.2	313	15	US-10-440-523-36	Sequence 36, Appl
22	75	12.3	275	12	US-10-282-122A-55250	Sequence 55250, A
23	74	12.1	363	14	US-10-349-508-39	Sequence 39, Appl
24	74	12.1	363	15	US-10-437-169-2	Sequence 39, Appl
25	74	12.1	363	15	US-10-471-243-22	Sequence 22, Appl
26	74	12.1	422	14	US-10-272-490-88	Sequence 22, Appl
27	70	11.4	460	14	US-10-214-473-40	Sequence 88, Appl
28	70	11.4	460	14	US-10-272-490-40	Sequence 40, Appl
29	69	11.3	520	14	US-10-032-201B-305	Sequence 40, Appl
30	69	11.3	524	14	US-10-032-201B-303	Sequence 305, Appl
31	69	11.3	528	14	US-10-032-201B-304	Sequence 303, Appl
32	68	11.1	115	15	US-10-108-260A-3222	Sequence 304, Appl
33	68	11.1	213	9	US-09-738-626-4741	Sequence 3222, Ap
34	68	11.1	216	9	US-09-935-757-2	Sequence 4741, Ap
35	68	11.1	216	9	US-09-935-757-6	Sequence 2, Appl
36	68	11.1	1321	16	US-10-408-765A-2241	Sequence 6, Appl
37	67	10.9	206	14	US-10-192-988-19	Sequence 2241, Ap
38	67	10.9	432	14	US-10-214-473-28	Sequence 19, Appl
39	67	10.9	432	14	US-10-272-490-28	Sequence 28, Appl
40	66	10.8	196	13	US-10-081-281-109	Sequence 109, Appl
41	66	10.8	441	13	US-10-015-536-17	Sequence 17, Appl
42	66	10.8	448	13	US-10-081-281-111	Sequence 11, Appl
43	66	10.8	500	9	US-09-766-378A-25	Sequence 25, Appl
44	66	10.8	562	9	US-09-815-837-70	Sequence 70, Appl
45	66	10.8	702	12	US-10-282-122A-78032	Sequence 78032, A

ALIGNMENTS

RESULT 1
US-09-796-692-666
Sequence 666, Application US/09796692
Publication No. US20020198362A1
GENERAL INFORMATION:
APPLICANT: Galger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
FILE REFERENCE: 2077, 001200
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: US/09/796, 692
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/196, 126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/190, 479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/200, 545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/200, 303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200, 779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200, 999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/202, 084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/206, 201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: 60/218, 950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/222, 903
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 60/223, 416
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: 60/223, 378
PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 9597

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! SOFTWARE: FastSeq for Windows Version 3.0
! SEQ ID NO 666
! LENGTH: 114
! TYPE: PRT
! ORGANISM: Homo sapiens
US-09-796-692-666
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Best Local Similarity 100.0%; Pred. No. 9.7e-65;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2

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US-10-040-862-666
; Sequence 666, Application US/10040862
; Publication No. US20030078396A1
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GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
FILE REFERENCE: 014058-013520US
CURRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: US/10/040,862
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/223,416
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: US 60/223,378
PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: US 09/796,692
PRIOR FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 666
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
US-10-040-862-666
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Query Match          100.0%; Score 612; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 9.7e-65;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 AECPTLGEAVTDHPDRLNAMEKEFYVLDKQHAMLPITTEIKDRLQLRVLLRREDVVLGRP 60
        |||
        2 AECPTLGEAVTDHPDRLNAMEKEFYVLDKQHAMLPITTEIKDRLQLRVLLRREDVVLGRP 61
DB      61 MPTQIGPSLLPIMMQLYPDGRYSSDSSFWRVLVYHIKIDGVEDMLLELPDD 113
        |||
        62 MPTQIGPSLLPIMMQLYPDGRYSSDSSFWRVLVYHIKIDGVEDMLLELPDD 114
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RESULT 3

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US-10-057-475B-666
; Sequence 666, Application US/10057475B
; Publication No. US2004002068A1
```

```
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Clapper, Jonathan David
APPLICANT: Wang, Aijun
APPLICANT: Ordonez, Nadia
APPLICANT: Carter, Lauren
APPLICANT: McNeill, Patricia Dianne
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
FILE REFERENCE: 014058-014402US
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: US/10/057,475B
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR FILING DATE: 2000-08-03
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 10979
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 666
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
US-10-057-475B-666
```

```
Query Match          100.0%; Score 612; DB 15; Length 114;
Best Local Similarity 100.0%; Pred. No. 9.7e-65;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 AECPTLGEAVTDHPDRLNAMEKEFYVLDKQHAMLPITTEIKDRLQLRVLLRREDVVLGRP 60
        |||
        2 AECPTLGEAVTDHPDRLNAMEKEFYVLDKQHAMLPITTEIKDRLQLRVLLRREDVVLGRP 61
DB      61 MPTQIGPSLLPIMMQLYPDGRYSSDSSFWRVLVYHIKIDGVEDMLLELPDD 113
        |||
        62 MPTQIGPSLLPIMMQLYPDGRYSSDSSFWRVLVYHIKIDGVEDMLLELPDD 114
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RESULT 4

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US-10-154-884B-666
; Sequence 666, Application US/10154884B
```

```
/ Publication No. US20040005561A1
/ GENERAL INFORMATION:
/ APPLICANT: Gaiger, Alexander
/ APPLICANT: Algate, Paul A.
/ APPLICANT: Mannion, Jane
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Corixa Corporation
/ TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
/ FILE REFERENCE: 014058-013521US
/ CURRENT APPLICATION NUMBER: US/10/154,884B
/ PRIOR FILING DATE: 2002-05-23
/ PRIOR APPLICATION NUMBER: US 60/186,126
/ PRIOR FILING DATE: 2000-03-01
/ PRIOR APPLICATION NUMBER: US 60/190,479
/ PRIOR FILING DATE: 2000-03-17
/ PRIOR APPLICATION NUMBER: US 60/200,545
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 60/200,303
/ PRIOR FILING DATE: 2000-04-28
/ PRIOR APPLICATION NUMBER: US 60/200,779
/ PRIOR FILING DATE: 2000-04-28
/ PRIOR APPLICATION NUMBER: US 60/200,999
/ PRIOR FILING DATE: 2000-05-01
/ PRIOR APPLICATION NUMBER: US 60/202,084
/ PRIOR FILING DATE: 2000-05-04
/ PRIOR APPLICATION NUMBER: US 60/206,201
/ PRIOR FILING DATE: 2000-05-22
/ PRIOR APPLICATION NUMBER: US 60/218,950
/ PRIOR FILING DATE: 2000-07-14
/ PRIOR APPLICATION NUMBER: US 60/222,903
/ PRIOR FILING DATE: 2000-08-03
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 11290
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 666
/ LENGTH: 114
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-154-884B-666

Query Match          100.0%; Score 612; DB 15; Length 114;
Best Local Similarity 100.0%; Pred. No. 9.7e-65;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AECPTLGAVTDPHRLWAMEKFFVYLDEKQHAWLPLTIEIKDRQLRVLLRREDVVLGRP 60
Db      2 AECPTLGAVTDPHRLWAMEKFFVYLDEKQHAWLPLTIEIKDRQLRVLLRREDVVLGRP 61
Qy      61 MTPQIGSLLPIMQOLYPDGRYRSSDSSFWRVLYVHIKIDGVEDMLLELPDD 113
Db      62 MTPQIGSLLPIMQOLYPDGRYRSSDSSFWRVLYVHIKIDGVEDMLLELPDD 114

RESULT 5
US-10-057-475B-10485
/ Sequence 10485, Application US/10057475B
/ Publication No. US20040002068A1
/ GENERAL INFORMATION:
/ APPLICANT: Gaiger, Alexander
/ APPLICANT: Algate, Paul A.
/ APPLICANT: Mannion, Jane
/ APPLICANT: Clapper, Jonathan David
/ APPLICANT: Wang, Aijun
/ APPLICANT: Ordenez, Nadia
/ APPLICANT: Carter, Lauren
/ APPLICANT: McNeill, Patricia Dianne
/ APPLICANT: Corixa Corporation
/ TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
/ FILE REFERENCE: 014058-014402US
/ CURRENT APPLICATION NUMBER: US/10/057,475B
/ CURRENT FILING DATE: 2002-01-22
```

```
/ PRIOR APPLICATION NUMBER: US 60/186,126
/ PRIOR FILING DATE: 2000-03-01
/ PRIOR APPLICATION NUMBER: US 60/190,479
/ PRIOR FILING DATE: 2000-03-17
/ PRIOR APPLICATION NUMBER: US 60/200,545
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 60/200,303
/ PRIOR FILING DATE: 2000-04-28
/ PRIOR APPLICATION NUMBER: US 60/200,779
/ PRIOR FILING DATE: 2000-04-28
/ PRIOR APPLICATION NUMBER: US 60/200,999
/ PRIOR FILING DATE: 2000-05-01
/ PRIOR APPLICATION NUMBER: US 60/202,084
/ PRIOR FILING DATE: 2000-05-04
/ PRIOR APPLICATION NUMBER: US 60/206,201
/ PRIOR FILING DATE: 2000-05-22
/ PRIOR APPLICATION NUMBER: US 60/218,950
/ PRIOR FILING DATE: 2000-07-14
/ PRIOR APPLICATION NUMBER: US 60/222,903
/ PRIOR FILING DATE: 2000-08-03
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 10979
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 10485
/ LENGTH: 121
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: His-TCL-1, TCL-1 with His tag
US-10-057-475B-10485

Query Match          100.0%; Score 612; DB 15; Length 121;
Best Local Similarity 100.0%; Pred. No. 1e-64;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AECPTLGAVTDPHRLWAMEKFFVYLDEKQHAWLPLTIEIKDRQLRVLLRREDVVLGRP 60
Db      9 AECPTLGAVTDPHRLWAMEKFFVYLDEKQHAWLPLTIEIKDRQLRVLLRREDVVLGRP 68
Qy      61 MTPQIGSLLPIMQOLYPDGRYRSSDSSFWRVLYVHIKIDGVEDMLLELPDD 113
Db      69 MTPQIGSLLPIMQOLYPDGRYRSSDSSFWRVLYVHIKIDGVEDMLLELPDD 121

RESULT 6
US-10-154-884B-10485
/ Sequence 10485, Application US/10154884B
/ Publication No. US20040005561A1
/ GENERAL INFORMATION:
/ APPLICANT: Gaiger, Alexander
/ APPLICANT: Algate, Paul A.
/ APPLICANT: Mannion, Jane
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Corixa Corporation
/ TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
/ FILE REFERENCE: 014058-013521US
/ CURRENT APPLICATION NUMBER: US/10/154,884B
/ PRIOR FILING DATE: 2002-05-23
/ PRIOR APPLICATION NUMBER: US 60/186,126
/ PRIOR FILING DATE: 2000-03-01
/ PRIOR APPLICATION NUMBER: US 60/190,479
/ PRIOR FILING DATE: 2000-03-17
/ PRIOR APPLICATION NUMBER: US 60/200,545
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 60/200,303
/ PRIOR FILING DATE: 2000-04-28
/ PRIOR APPLICATION NUMBER: US 60/200,779
/ PRIOR FILING DATE: 2000-04-28
/ PRIOR APPLICATION NUMBER: US 60/200,999
/ PRIOR FILING DATE: 2000-05-01
/ PRIOR APPLICATION NUMBER: US 60/202,084
/ PRIOR FILING DATE: 2000-05-04
```

```
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10485
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: His-TCL-1, TCL-1 with His tag
US-10-154-884B-10485

Query Match          100.0%; Score 612; DB 15; Length 121;
Best Local Similarity 100.0%; Pred. No. 1e-64;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 AECPTLGEAVTDHPDRLMAWEKFFVYLDEKQAHMLPTTIEIKDRLQRLVLLRREDVVLGR 60
    |||
Db 9 AECPTLGEAVTDHPDRLMAWEKFFVYLDEKQAHMLPTTIEIKDRLQRLVLLRREDVVLGR 68
    |||

Cy 61 MTPPIGSLPPIPMQLYPDGRYSSDSSFWRVLYTHIKIDGVEDMLLELPDD 113
    |||
Db 69 MTPPIGSLPPIPMQLYPDGRYSSDSSFWRVLYTHIKIDGVEDMLLELPDD 121
    |||

RESULT 7
US-09-796-692-1528
; Sequence 1528, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1528
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
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```
US-09-796-692-1528

Query Match          52.0%; Score 318; DB 9; Length 76;
Best Local Similarity 100.0%; Pred. No. 5.4e-30;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 AECPTLGEAVTDHPDRLMAWEKFFVYLDEKQAHMLPTTIEIKDRLQRLVLLRREDVVLGR 59
    |||
Db 18 AECPTLGEAVTDHPDRLMAWEKFFVYLDEKQAHMLPTTIEIKDRLQRLVLLRREDVVLGR 76
    |||

RESULT 8
US-10-040-862-1528
; Sequence 1528, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1528
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-040-862-1528

Query Match          52.0%; Score 318; DB 14; Length 76;
Best Local Similarity 100.0%; Pred. No. 5.4e-30;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 AECPTLGEAVTDHPDRLMAWEKFFVYLDEKQAHMLPTTIEIKDRLQRLVLLRREDVVLGR 59
    |||
Db 18 AECPTLGEAVTDHPDRLMAWEKFFVYLDEKQAHMLPTTIEIKDRLQRLVLLRREDVVLGR 76
    |||

RESULT 9
US-10-057-475B-1528
; Sequence 1528, Application US/10057475B
; Publication No. US20040002068A1
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ORGANISM: Proteu
US-10-282-122A-68466

QY 70 LLPIMWOLYPDGRY 83

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Db          499 ILPIWMSLEPHHRY 512

RESULT 14
US-10-282-122A-73477
: Sequence 73477, Application US/10282122A
: Publication No. US20040029129A1
: GENERAL INFORMATION:
:   APPLICANT: Wang, Lianguo
:   APPLICANT: Zamudio, Carlos
:   APPLICANT: Malone, Cheryl
:   APPLICANT: Haselbeck, Robert
:   APPLICANT: Ohlsen, Kari
:   APPLICANT: Zykied, Judith
:   APPLICANT: Wall, Daniel
:   APPLICANT: Trawick, John
:   APPLICANT: Carr, Grant
:   APPLICANT: Yamamoto, Robert
:   APPLICANT: Foreyeth, R.
:   APPLICANT: Xu, H.
: TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
: FILE REFERENCE: ELITRA.034A
: CURRENT APPLICATION NUMBER: US/10/282,122A
: CURRENT FILING DATE: 2003-02-20
: PRIOR APPLICATION NUMBER: 60/191,078
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: 60/206,848
: PRIOR FILING DATE: 2000-05-23
: PRIOR APPLICATION NUMBER: 60/207,727
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: 60/230,335
: PRIOR FILING DATE: 2000-09-06
: PRIOR APPLICATION NUMBER: 60/230,347
: PRIOR FILING DATE: 2000-09-09
: PRIOR APPLICATION NUMBER: 60/242,578
: PRIOR FILING DATE: 2000-10-23
: PRIOR APPLICATION NUMBER: 60/253,625
: PRIOR FILING DATE: 2000-11-27
: PRIOR APPLICATION NUMBER: 60/257,931
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 60/267,636
: PRIOR FILING DATE: 2001-02-09
: PRIOR APPLICATION NUMBER: 60/269,308
: PRIOR FILING DATE: 2001-02-16
: Remaining Prior Application data removed - See file wrapper or PALM.
: NUMBER OF SEQ ID NOS: 78614
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 73477
: LENGTH: 619
: TYPE: PRT
: ORGANISM: Salmonella paratyphi A
: FEATURE:
:   NAME/KEY: MISC FEATURE
:   LOCATION: (611)..(611)
:   OTHER INFORMATION: X=any amino acid
US-10-282-122A-73477

Query Match          14.1%; Score 86; DB 12; Length 619;
Best Local Similarity 29.7%; Pred. No. 0.3;
Matches 22; Conservative 20; Mismatches 26; Indels 6; Gaps 3

QY      16 RLWAW---EKFYVLDEKQAHMLPL-TIEIKDRLQLRLRLREDVVLGRPM-TPTQIGPS 69
: ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      431 KTWAMETAMEGIDREVSERTEVAAVPIRGTGHPNEVRLIDVLLRPEVLVEPELMTVIPIGKA 490
QY      70 LLPTMQLYPEDGRY 83
: ||| : : : : : : : : : : : : : : : : : : : : : : : : :
Db      491 ILPIWMSLEPHHRY 504

RESULT 15
US-10-282-122A-43135
: Sequence 43135, Application US/10282122A

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/ Publication No. US20040023129A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Liangsu
/ APPLICANT: Zamudio, Carlos
/ APPLICANT: Malone, Cheryl
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Kari
/ APPLICANT: Zykend, Judith
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John
/ APPLICANT: Carr, Grant
/ APPLICANT: Yamamoto, Robert
/ APPLICANT: Forsyth, R.
/ APPLICANT: Xu, H.
/ TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
/ FILE REFERENCE: EUTRA.034A US/10/282,122A
/ CURRENT FILING DATE: 2003-02-20
/ PRIOR APPLICATION NUMBER: 60/119,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/230,335
/ PRIOR FILING DATE: 2000-09-06
/ PRIOR APPLICATION NUMBER: 60/230,347
/ PRIOR FILING DATE: 2000-09-09
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/267,636
/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 78614
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 43135
/ LENGTH: 619
/ TYPE: PR1
/ ORGANISM: Escherichia coli
US-10-282-122A-43135

Query Match 13.6%; Score 83; DB 12; Length 619;
Best Local Similarity 28.4%; Pred. No. 0.67;
Matches 21; Conservative 21; Mismatches 26; Indels 6; Gaps 3.

OY 16 RUMAME---KFVYDEKONHMLPL-TLEIKDRLOLRVLRREDVYIGRPW-TPTQIGPS 69
: ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 440 KTWAMEHAFDQIRKVSDBEFANVIFRIGHFONEVRLLIDVLREPLYVEPLMTVIQNKKA 499
: ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 70 LLPIMQLYDPGRY 83
: ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 500 ILPIIMSLFPHHRY 513

Search completed: June 17, 2004, 14:37:31
Job time : 503 secs

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This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 17, 2004, 14:25:11 ; Search time 22 Seconds
(without alignments)
265.170 Million cell updates/sec

Title: US-09-441-242a-2

Perfect score: 612

Sequence: 1 AECPTLGEAVTDHEDRLMAW.....VYHKKIDGVEDMLLELPDD 113

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/2/1aa/PCtus_COMB.pep:*
- 6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	612	100.0	113	2	US-08-330-272-2
2	612	100.0	113	5	PCT-US95-13663-2
3	221	36.1	108	2	US-08-330-272-4
4	221	36.1	108	5	PCT-US95-13663-4
5	91.5	15.0	639	4	US-09-543-681A-6148
6	83	13.6	621	4	US-09-549-848B-39
7	74	12.1	363	4	US-09-489-039A-9256
8	67	10.9	206	2	US-08-438-439C-19
9	66	10.8	256	3	US-08-484-905-113
10	66	10.8	256	3	US-08-481-985B-113
11	66	10.8	256	3	US-08-376-476-113
12	66	10.8	500	3	US-08-960-190A-25
13	65	10.6	712	4	US-09-489-039A-10736
14	64	10.5	194	4	US-09-107-532A-6568
15	64	10.5	344	4	US-09-198-452A-880
16	63.5	10.4	489	4	US-09-310-463-14
17	63.5	10.4	489	4	US-08-842-248A-14
18	63.5	10.4	906	1	US-08-220-151-9
19	63.5	10.4	906	1	US-08-413-118-9
20	63.5	10.4	906	3	US-08-473-446-9
21	63.5	10.4	1019	1	US-08-296-014A-4
22	63.5	10.4	1019	2	US-08-596-405-4
23	63.5	10.4	1019	2	US-08-877-620-4
24	63.5	10.4	1019	4	US-09-287-368-4
25	63.5	10.4	1083	1	US-08-296-014A-2
26	63.5	10.4	1083	2	US-08-596-405-2
27	63.5	10.4	1083	2	US-08-877-620-2

28	63.5	10.4	1083	4	US-09-287-368-2	Sequence 2, Appli
29	62.5	10.2	382	4	US-09-489-039A-8323	Sequence 8323, Ap
30	62	10.1	509	2	US-08-890-980-2	Sequence 2, Appli
31	62	10.1	509	3	US-08-890-979-2	Sequence 2, Appli
32	62	10.1	509	3	US-09-032-894-2	Sequence 2, Appli
33	62	10.1	509	3	US-09-031-626-2	Sequence 2, Appli
34	62	10.1	703	4	US-09-252-991A-23905	Sequence 23905, A
35	61.5	10.0	713	1	US-08-453-472-6	Sequence 6, Appli
36	61.5	10.0	713	1	US-08-038-948-7	Sequence 7, Appli
37	61.5	10.0	713	1	US-08-038-948-8	Sequence 8, Appli
38	61.5	10.0	713	1	US-08-038-948-10	Sequence 10, Appli
39	61.5	10.0	713	1	US-08-453-952-6	Sequence 6, Appli
40	61.5	10.0	713	2	US-08-862-903-6	Sequence 6, Appli
41	61	10.0	222	4	US-09-252-991A-22189	Sequence 22189, A
42	61	10.0	546	3	US-09-252-991A-27705	Sequence 27705, A
43	61	10.0	785	3	US-09-265-108-2	Sequence 2, Appli
44	61	10.0	785	3	US-09-479-264-2	Sequence 2, Appli
45	61	10.0	1279	4	US-09-489-039A-13602	Sequence 13602, A

ALIGNMENTS

RESULT 1
US-08-330-272-2
Sequence 2, Application US/08330272
Patent No. 5985598
GENERAL INFORMATION:
APPLICANT: Russco et al
TITLE OF INVENTION: TCL-1 Gene and Protein and Related
TITLE OF INVENTION: Methods and Compositions
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennine & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/330,272
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Matarock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6754-027
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 790-8864/9741
TELEX: 66141 PENNINE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-330-272-2
Query Match 100.0%; Score 612; DB 2; length 113;
Best Local Similarity 100.0%; Pred. No. 8.1e-71;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 AECPTLGEAVTDHEDRLMAWEKFFYLDKQNAWPLTTEIKDRLOQLRLRRDVTGCRP 60
Db 1 AECPTLGEAVTDHEDRLMAWEKFFYLDKQNAWPLTTEIKDRLOQLRLRRDVTGCRP 60
Cy 61 MTPQIGPSLLPIWMOGLYPDGGRYSSDSFWRVLVYHKKIDGVEDMLLELPDD 113

Db 61 MPTQIGPSLPIIMQLYPDGRYSSDSFMRVYHIKIDGVEDMLLELPDD 113

RESULT 2
PCT-US95-13663-2
Sequence 2, Application PC/TUS9513663
GENERAL INFORMATION:
APPLICANT: Russo et al
TITLE OF INVENTION: TCU-1 Gene and Protein and Related
TITLE OF INVENTION: Methods and Compositions
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13663
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6754-027
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 790-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-13663-2

Query Match 100.0%; Score 612; DB 5; Length 113;
Best Local Similarity 100.0%; Pred. No. 8, 1e-71;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 AECPTLGBAVTDHPDRIMAMEKFVYLDEKOHAMLPITIEIKDRLQLRVLRRREDVVLGRP 60
1 AECPTLGBAVTDHPDRIMAMEKFVYLDEKOHAMLPITIEIKDRLQLRVLRRREDVVLGRP 60

Db 61 MPTQIGPSLPIIMQLYPDGRYSSDSFMRVYHIKIDGVEDMLLELPDD 113
61 MPTQIGPSLPIIMQLYPDGRYSSDSFMRVYHIKIDGVEDMLLELPDD 113

RESULT 3
US-08-330-272-4
Sequence 4, Application US/08330272
Patent No. 5985598
GENERAL INFORMATION:
APPLICANT: Russo et al
TITLE OF INVENTION: TCU-1 Gene and Protein and Related
TITLE OF INVENTION: Methods and Compositions
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/330,272
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6754-027
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 790-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-330-272-4

Query Match 36.1%; Score 221; DB 2; Length 108;
Best Local Similarity 40.2%; Pred. No. 1, 1e-20;
Matches 43; Conservative 23; Mismatches 39; Indels 2; Gaps 1;

Db 7 GEAVTDHPDRIMAMEKFVYLDEKOHAMLPITIEIKDRLQLRVLRRREDVVLGRPMPPTOI 66
3 GEVGAHPDRIMVHOGITRDEYQRTWVAVVEETSFLEARY--QIQVPLGDAARPSHI 60

Db 67 GPSLPIIMQLYPDGRYSSDSFMRVYHIKIDGVEDMLLELPDD 113
61 LTSQLPIIMQLYPEERYMDNNSRLMQIOHHLWVRGVQELLKLLPDD 107

RESULT 4
PCT-US95-13663-4
Sequence 4, Application PC/TUS9513663
GENERAL INFORMATION:
APPLICANT: Russo et al
TITLE OF INVENTION: TCU-1 Gene and Protein and Related
TITLE OF INVENTION: Methods and Compositions
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13663
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6754-027
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 790-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

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; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
;
PCT-US95-13663-4

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Query Match	36.1%	Score 221	DB 5	Length 108
Best Local	40.2%	Pred. No. 1.1e-20		
Matches 43	Conservative 23	Mismatches 39	Indels 2	Gaps 1

Qy 7 GEALVDHPDRIMAMEKRVYLDEQHAMLPITIEIKDRLQIRVLLRREDVVGKRPMTPTQI 66
|||:::||::|||:
Db 3 GEDVGA^RPRDLHVMHQEIGYRDEYQRTWVAVEETSFLKARV--QQIQVPLGDANPSHL 600

```
Oy      |67 GPSLLPIMWQLYPDGRKYRSSDSSFVKLVYHIKIDGVEDMLELPPDD    113  
        |||::|||:::||::|||::|||  
Db      |61 LTSQPLMWQLYPEERYMDNNSRLMGIQHILMVRSVGLLEKLKPDD     107
```

RESULT 5
US-09-543-681A-6148
; Sequence 6148, Application US/09543681A

: APPLICANT: GARY BRETON
 : TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
 : TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

CURRENT FILING DATE: 2000-04-05
 PRIOR APPLICATION NUMBER: US 60/128,706
 PRIOR FILING DATE: 1999-04-09

```

; SEQ ID NO 6148
;
; LENGTH: 639
;
; TYPE: PR1
;
; ORGANISM: Proteus mirabilis
;
US-09-543-681A-6148

```

Query Match 15.0%; Score 91.5; DB 4; Length 639;
Best Local Similarity 33.3%; Pred. No. 0.0051;
Matches 26; Conservative 13; Mismatches 24; Indels 15; Gaps 4;

QY 16 RLWMEKFVYLDE----KQHWLPLTI----EIQRLQLRVLLREEDVLTGRPMPTQ 65
: ||| ||: : : : ||: : ||| |
Db 455 KTWAME--TALDQLRESESQSLPIRIGDPAGEVR---LVVYLLREITVEEPLWILIP 509

```
QY      66 IGPSLPIMWQLYPDGRY 83
      ::|||:||||:|
Db      510 SNKALPILWQLFPDNPY 527
```

RESULT 6
US-09-489-039A-9256
; Sequence 9256, Application US/09489039A

; APPLICANT: Gary Breton et. al
 ; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES RELATING TO KLEBSIELLA
 ; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
 ; TITLE OF INVENTION:

; CURRENT APPLICATION NUMBER: US/09/489, 039A
 ; CURRENT FILING DATE: 2000-01-27
 ; PRIOR APPLICATION NUMBER: US 60/117, 747

```

; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9256
; LENGTH: 621

```

ORGANISM: *Klebsiella pneumoniae*
US-09-489-039A-9256

Query Match	13.6%;	Score 83;	DB 4;	Length 621;
Best Local Similarity	27.0%;	Pred. No. 0.06;		
Matches	20;	Conservative	22;	Mismatches 26;
				Indels 6;
				Gaps 3;

```

Oy      16 RLNAMEKPY---YLDEKOHAMLPY-TIEIKDRLOLRVLLRRDDVVLGRPM-TPTQIGPS 69
        : ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      440 KTNAMETALBQVREVSAAEEVAAPVIRTHGPQNEVALLDVLLRPEVLVEEPLMTVIPSKNA 499

```

QY	70	LPIMWQLYPDGRY	83
	:	:: :	
Db	500	ILPVLWSLFPHHRY	513

RESULT 7
US-09-549-848B-39
; Sequence 39, Application US/09549848B

```
; APPLICANT: Lassner, Michael
; APPLICANT: Post-Beitenmiller, Dusty
; APPLICANT: Savidge, Beth
```

REFERENCE: 16259 United States
 TITLE OF INVENTION: Nucleic Acid Sequences Involved in
 TITLE OF INVENTION: Tocopherol Synthesis
 FILE REFERENCE: 17133/02/US
 CURRENT APPLICATION NUMBER: US/09/549,848B

PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: 60/146,461
PRIOR FILING DATE: 1999-07-30

```

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 363
; TYPE: PRT

```

; ORGANISM: *Synechocystis* sp.
US-09-549-848B-39

Query Match	12.1%	Score 74;	DB 4;	Length 363;
Best Local Similarity	25.0%	Pred. No. 0.42;		
Matches	26;	Conservative	15;	Mismatches 31;
				Indels 32;
				Gaps 6;

```

QY      14 PDLIMAMEKEFVYIDKONHMLPTLTIEIKRQLRLVLRREDVVLGRPMPT----- 64
      | | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | |
Db      211 PSR-WFWIQANYPPD--HPSLSVYAAAGG-----IVLGRPEEVALIGLHHQGN 256

```

QY	65	-QIGPSLLPI	MMQLY	PDGRY--	RSSDS	FWRLV	YHIK	IGVED	104
		:	:	:	:	:	:	:	
DB	257	FYEFGPGH	CTVT	MQVAP	FWGRMQL	KASND	RYW----	VKLSG	KT
		:	:	:	:	:	:	:	
		:	:	:	:	:	:	:	295

RESULT 8
US-08-438-439C-19
; Sequence 19, Application US/08438439C

APPLICANT: Nathans, Jeremy
APPLICANT: Smallwood, Phillip M.
APPLICANT: Macke, Jennifer P.

NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.

CITY: La Jolla
STATE: CA
COUNTRY: USA

```

;          2007
;
;  COMPUTER READABLE FORM:
;    MEDIUM TYPE:  Floppy disk
;  COMPUTER:  IBM PC compatible

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Fr1 Jun 18 14:20:09 2004

us-09-441-242a-2.rai

Page 3

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,439C
FILING DATE: May 12, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/046001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 206 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-438-439C-19

Query Match 10.9%; Score 67; DB 2; Length 206;
Best Local Similarity 24.1%; Pred. No. 1.5;
Matches 26; Conservative 6; Mismatches 30; Indels 46; Gaps 4;

QY 18 WAMEKPYLDEKHAMLPTEIKDRQLRLREDDVVGKRPMTPTQIGPSLLPIMW-- 75
DB 45 WMEISVAL--SLAMLPVAAQPK-----AAVQAGAGYLLGIRKMW 84

QY 76 -----QLYPDGRYSSDSFWRLYVYHIKIDGVEDMLLELP 111
DB 85 WLYNCVIGPHLQALPDGICGALADTW-----DSLLELP 120

RESULT 9
US-08-484-905-113
Sequence 113, Application US/08484905
Patent No. 5976551
GENERAL INFORMATION:
APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourileky, Philippe
TITLE OF INVENTION: An Altered Major Histocompatibility
TITLE OF INVENTION: Complex (MHC) Determinant and Methods for Using the
TITLE OF INVENTION: Determinant
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESS: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,905
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E. R.

REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 03495.0106-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 256 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-905-113

Query Match 10.8%; Score 66; DB 2; Length 256;
Best Local Similarity 22.2%; Pred. No. 2.8;
Matches 32; Conservative 24; Mismatches 30; Indels 58; Gaps 8;

QY 23 FYVLDKQKHAM-LPLTEIK-----DRQLRLREDD----- 54
DB 60 YVDLDKKEIVWMLPEFAQLRRFPQGLQNIATGKHLBITLRKSNSTPATNEAPQATVF 119

QY 55 -----VILGRPMT-----PTQIGPSLLPIMW-----QLYPDGRYSS-----DSFWRLL----- 93
DB 120 PKSPVLLGQENTLICEVDNIFPPVINITWLRNSKSVTDGVYETSFVYNRDYSFKLSYLT 179

QY 94 -----VYHIKID--GVEDMLLE 108
DB 180 FIPSDDIYDCKVEHMGLEBPVLK 203

RESULT 10
US-08-481-985B-113
Sequence 113, Application US/08481985B
Patent No. 601146
GENERAL INFORMATION:
APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourileky, Philippe
TITLE OF INVENTION: Altered Major Histocompatibility Complex
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESS: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,985B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0106-04000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 113:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 256 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-481-985B-113

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Query Match	10.8%	Score	66	DB	3	Length	256
Best Local Similarity	22.2%	Pred	No.	2.8			
Matches	32	Conservative	24	Mismatches	30	Indels	58
						Gaps	8

QY 23 FVYLDEKQAHM-LEPLTEIK-----DELQRYLLRED-----54
 Db 60 YVDLDKETVYMLPEPAQLRRPEPGGLIATGTHNLEILTKNSNSTPATNEAPQATVP 119
 QY 55 ----VVLGRPMT-----PTQIGSLPLIMV----QLPYDGRYSS----DSSFARL-----93
 Db 120 PKSPVLIGQENTITICFVDNIFFPVNIITWLRNSKSVTDGVIETSPFVNRIYSFKLSYLT 179
 QY 94 -----VYHIKID--GVEDMLLE 108
 Db 180 FIPSDDDIYDCKVEHNGLEPVIK 203

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1 RESULT 11
2 US-08-370-476-113
3 Sequence 113, Application US/08370476
4 Patent No. 6153408
5 GENERAL INFORMATION:
6 APPLICANT: Mottez, Estelle
7 APPLICANT: Abastado, Jean-Pierre
8 APPLICANT: Kourileky, Phillipe
9 APPLICANT: Lone, Yu-Chun
10 APPLICANT: Ojcius, David
11 APPLICANT: Casrouge, Armande
12 TITLE OF INVENTION: Altered Major Histocompatibility Complex
13 TITLE OF INVENTION:
14 NUMBER OF SEQUENCES: 127
15 CORRESPONDENCE ADDRESS:
16 ADDRESSER: Finegan, Henderson, Farabow, Garrett &
17 ADDRESSER: Dunner
18 STREET: 1300 I Street, N.W., Suite 700
19 CITY: Washington
20 STATE: D.C.
21 ZIP: 20005-3315
22 COMPUTER READABLE FORM:
23 MEDIUM TYPE: Floppy disk
24 COMPUTER: IBM PC compatible
25 OPERATING SYSTEM: PC-DOS/MS-DOS
26 SOFTWARE: PatentIn Release #1.0, Version #1.25
27 CURRENT APPLICATION DATA:
28 APPLICATION NUMBER: US/08/370,476
29 FILING DATE:
30 CLASSIFICATION: 435
31 PRIOR APPLICATION DATA:
32 APPLICATION NUMBER: US 08/117,575
33 FILING DATE: 07-SEP-1993
34 APPLICATION NUMBER: US 08/072,787
35 FILING DATE: 06-JUN-1993
36 PRIOR APPLICATION DATA:
37 APPLICATION NUMBER: US 07/801,818
38 FILING DATE: 05-DEC-1991
39 PRIOR APPLICATION DATA:
40 APPLICATION NUMBER: US 07/792,473
41 FILING DATE: 15-NOV-1991
42 ATTORNEY/AGENT INFORMATION:
43 NAME: Meyers, Kenneth J.
44 REGISTRATION NUMBER: 25,146
45 REFERENCE/DOCKET NUMBER: 05243.0001-01000
46 TELECOMMUNICATION INFORMATION:
47 TELEPHONE: 202-408-4000
48 TELEFAX: 202-408-4400
49 INFORMATION FOR SEQ ID NO: 113:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 256 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-370-476-113

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Query Match	10.8%	Score 66	DB 3	Length 256
Best Local Similarity	22.2%	Pred. NC. 2.8		
Matches 32		Conservative 24	Mismatches 30	Indels 58
				Gaps 8

[illegible]

RESULT 12
 US-08-960-190A-25
 Sequence 25, Application US/08960190A
 Patent No. 6232445
 GENERAL INFORMATION:
 APPLICANT: Rhode, Peter R.
 APPLICANT: Acevedo, Jorge
 APPLICANT: Burkhardt, Martin
 APPLICANT: Jiao, Jin-an
 APPLICANT: Wong, Hing C.
 TITLE OF INVENTION: SOLUBLE MHC COMPLEXES AND
 TITLE OF INVENTION: METHODS OF USE THEREOF
 NUMBER OF SEQUENCES: 38
 CORRESPONDENCE ADDRESSES:
 ADDRESSES: Dike, Bronstein, Roberts & Cushman, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: usa
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/960,190A
 FILING DATE: 29-OCT-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Cortless, Peter F
 REGISTRATION NUMBER: 33,860
 REFERENCE/DOCKET NUMBER: 48002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 TELEX:
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 500 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 US-08-960-190A-25

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      APPLICATION NUMBER: US/09/107,5532A
      FILING DATE: 30-Jun-1998
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: 60/065,598
      FILING DATE: 14 May 1998
      APPLICATION NUMBER: 60/051571
      FILING DATE: July 2, 1997
      ATTORNEY/AGENT INFORMATION:
      NAME: Ariniello, Pamela Deneké
      REGISTRATION NUMBER: 40,489
      REFERENCE/DOCKET NUMBER: GTC-012
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (781)893-5007
      TELEFAX: (781)893-8277
      INFORMATION FOR SEQ ID NO: 6568:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 194 amino acids
      TYPE: amino acid
      TOPOLOGY: linear
      MOLECULE TYPE: protein
      HYPOTHETICAL: YES
      ORIGINAL SOURCE:
      ORGANISM: Enterococcus faecium
      FEATURE:
      NAME/KEY: misc feature
      LOCATION: (b) LOCATION 1..194
      SEQUENCE DESCRIPTION: SEQ ID NO: 6568:
      US-09-107-5532A-6568

      Query Match      10.5%; Score 64; DB 4; Length 194;
      Best Local Similarity 26.8%; Pred. No. 3.4;
      Matches 30; Conservative 14; Mismatches 34; Indels 34; Gaps 9;

      QY      7      GEAVTDHPRLWAMEKFVYLD-EKOHAMLPITIEIKRIQLRLVLRREDVYLGKPTPTQ 65
      DB      59      GGTATDHP---LIEDTYIEVDLENQHMWY-----YKDG---KVAL-ETDIVSGKPTTPT- 105
      QY      66      IGPSLDPTMWQ-----LYPDGRYRSSDSFRLVNHKIKD---GYED 104
      DB      106     --PAGVFVWNKEEDATLTKGTNDGTPYSPFVNVW-----MPLDWTGVGIHD 150

      RESULT 15
      US-09-198-452A-880
      ; Sequence 880, Application US/09198452A
      ; Patent No. 6559294
      ; GENERAL INFORMATION:
      ; APPLICANT: Griffaia, R.
      ; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
      ; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
      ; FILE REFERENCE: 9710-003-999
      ; CURRENT APPLICATION NUMBER: US/09/198,452A
      ; CURRENT FILING DATE: 1998-11-24
      ; NUMBER OF SEQ ID NOS: 6849
      ; SEQ ID NO 880
      ; LENGTH: 344
      ; TYPE: PRT
      ; ORGANISM: Chlamydia pneumoniae
      US-09-198-452A-880

      Query Match      10.5%; Score 64; DB 4; Length 344;
      Best Local Similarity 31.4%; Pred. No. 7.4;
      Matches 27; Conservative 11; Mismatches 24; Indels 24; Gaps 5;

      QY      4      PTLGAAYVDHPD-----RLWAME-----KFVYIDKQHAMLPV-----TIEIKDR 43
      DB      233     PLLAEAVLDHPAYRETSILRDGIWEAVKRGQAHAIQEHQAALAELEFKTRDPRLELRDK 292
      QY      44      IQLRVTLREEDV--VLGRPMPTPTQIG 67
      DB      293     MOL--LLSRVDLLPLLNKKMPDYTLIG 316
  
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Search completed: June 17, 2004, 14:29:00
Job time : 23 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 17, 2004, 11:25:55 ; Search time 3768 Seconds
(without alignments)
10492.974 Million cell updates/sec

Title: US-09-441-242a-1
Perfect score: 1324
Sequence: 1 ctgagagagcctgctctt.....catgagaaaaaaaaaaaaa 1324

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estcov:*
6: em_estpl:*
7: em_estro:*
8: em_hcc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hcc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_dhg:*
27: em_gss_vrt1:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	962	72.7	1029	9	AL560721 AL560721
2	952	71.9	1023	9	AL560722 AL560722
3	941.4	71.1	1201	13	BX421512 BX421512
4	921	69.6	1043	12	BM927381 BM927381

5	905.4	68.4	1031	13	BQ061021	BQ061021	AGENCOURT
6	903	68.2	985	13	BQ062796	BQ062796	AGENCOURT
7	889.8	67.2	986	13	BQ065603	BQ065603	AGENCOURT
8	886.6	67.0	1029	13	BQ061232	BQ061232	AGENCOURT
9	881.4	66.6	982	13	BQ056675	BQ056675	AGENCOURT
10	877.8	66.3	964	12	BQ754764	BQ754764	AGENCOURT
11	875	66.1	1056	13	BM927621	BM927621	AGENCOURT
12	870.4	65.7	988	13	BQ064806	BQ064806	AGENCOURT
13	858.2	64.8	990	13	BQ059785	BQ059785	AGENCOURT
14	858.2	64.8	990	13	BQ059785	BQ059785	AGENCOURT
15	856.6	64.7	1038	12	BM927418	BM927418	AGENCOURT
16	849.2	64.1	1004	13	BX407882	BX407882	AGENCOURT
17	847.8	64.0	983	13	BQ061991	BQ061991	AGENCOURT
18	845	63.8	990	13	BQ058531	BQ058531	AGENCOURT
19	834	63.0	1037	13	BQ055518	BQ055518	AGENCOURT
20	833.2	62.9	1026	13	BQ061686	BQ061686	AGENCOURT
21	832.4	62.9	905	13	BQ082730	BQ082730	AGENCOURT
22	829.2	62.6	963	13	BQ063405	BQ063405	AGENCOURT
23	826.6	62.4	984	13	BQ057145	BQ057145	AGENCOURT
24	826.4	62.4	894	12	BQ758818	BQ758818	AGENCOURT
25	826.2	62.4	1073	13	BQ065790	BQ065790	AGENCOURT
26	825.8	62.4	1030	13	BQ061108	BQ061108	AGENCOURT
27	823.8	62.2	988	13	BQ060743	BQ060743	AGENCOURT
28	823	62.2	1002	13	BX407883	BX407883	AGENCOURT
29	822.8	62.1	1030	13	BQ066787	BQ066787	AGENCOURT
30	819.8	61.9	1001	13	BQ060857	BQ060857	AGENCOURT
31	818.2	61.8	952	13	BQ064150	BQ064150	AGENCOURT
32	815.8	61.6	876	13	BX435946	BX435946	AGENCOURT
33	813.8	61.5	975	12	BQ759376	BQ759376	AGENCOURT
34	813.6	61.5	982	13	BQ061994	BQ061994	AGENCOURT
35	811.2	61.3	916	12	BQ757301	BQ757301	AGENCOURT
36	807.8	61.0	1040	13	BQ056512	BQ056512	AGENCOURT
37	804.8	60.8	963	13	BQ063369	BQ063369	AGENCOURT
38	802.8	60.6	1004	13	BQ064800	BQ064800	AGENCOURT
39	796	60.1	883	13	BX443335	BX443335	AGENCOURT
40	795	60.0	863	12	BM051836	BM051836	AGENCOURT
41	794	60.0	1018	13	BQ063070	BQ063070	AGENCOURT
42	793.8	60.0	927	13	BQ643245	BQ643245	AGENCOURT
43	793.6	59.9	1022	12	BQ054660	BQ054660	AGENCOURT
44	793	59.9	978	13	BQ057729	BQ057729	AGENCOURT
45	790.8	59.7	795	12	B1226543	B1226543	AGENCOURT

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION AL560721 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
Homo sapiens CDNA clone CSODL004TM02 3-PRIME, mRNA sequence.
ACCESSION AL560721
VERSION AL560721.2 GI:31284850
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Ll.W.B., Gruber,C., Jessee,J. and Polayes,D.
JOURNAL Full-length cDNA libraries and normalization
COMMENT Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:12907452.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7222.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODL004G01NP1cluster=7222.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DL004BG01NP1.
 Location/Qualifiers

FEATURES

source

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DL004YM02"
/cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
/cell_line="RAMOS CELL LINE"
/clone_11b="Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
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ORIGIN

Query Match 72.7%; Score 962; DB 9; Length 1029;
 Best Local Similarity 97.8%; Pred. No. 1.6e-189;
 Matches 1009; Conservative 8; Mismatches 10; Indels 5; Gaps 4;

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OY 155 TAAACATGAGATAAAGATAGTTACGTTACGGGTCTCTTGGTGGGAAGACGTG 214
Db 1029 TAAACATGAGATAAAGATAGTTACGTTACGGGTCTCTTGGTGGGAAGACGTG 970
OY 215 TCTTGGGAGGCGCTATGACCCCGACGATAGCGCCAGCGTGTGCTTCAATTTGGC 274
Db 969 TCTTGGGAGGCGCTATGACCCCGACGATAGCGCCAGCGTGTGCTTCAATTTGGC 912
OY 275 AGCTTACCTTGATGAGATACCGATCTGAGATCTTCAGTTCTTGCGCTTAACTGATAC 334
Db 911 AGCTTACCTTGATGAGATACCGATCTGAGATCTTCAGATCTTCAAGTGTGCGCTTAACTGATAC 852
OY 335 ACATCAAAATGACGCGCTGAGAGACATGCTTCTGAGACTGCTGCCAGATACATGATGA 394
Db 851 ACATCAAAATGACGCGCTGAGAGACATGCTTCTGAGACTGCTGCCAGATACATGATGA 792
OY 395 TGGTCTTGGAGACACCTGTCTCTTCA-CCCGAGGCGCTAGCGCTGGCCGACCTACAT 453
Db 791 TGGTCTTGGAGACACCTGTCTCTTCA-CCCGAGGCGCTAGCGCTGGCCGACCTACAT 732
OY 454 GGGGATGTTGTTCTGTTTCACTTCTGTTACTAGCTGTGCTTCTTCCACCACTG 513
Db 731 GGGGATGTTGTTCTGTTTCACTTCTGTTACTAGCTGTGCTTCTTCCACCACTG 672
OY 514 GGGTCTGGGAGAGATGACAGACAGAGATAGCTTACCCAGGCGCTGACGAGACTGCC 573
Db 671 GGGTCTGGGAGAGATGACAGACAGAGATAGCTTACCCAGGCGCTGACGAGACTGCC 612
OY 574 TGTAGCCCACTCTGCTGCTTACCACTACCTCTGCGCAAGAGATTCCATTTGACA 633
Db 611 TGTAGCCCACTCTGCTGCTTACCACTACCTCTGCGCAAGAGATTCCATTTGACA 552
OY 634 GAGCTTCTTCAAGTGGCCAGCTTACCTGTGCTCGCTTTTCTCACTGATGATGAT 693
Db 551 GAGCTTCTTCAAGTGGCCAGCTTACCTGTGCTCGCTTTTCTCACTGATGATGAT 492
OY 694 CTTAGAGCTCTTTTGTGCTTCTGCTTCTGCTTCAAGCACTGATTTTATTTGACACCC 753
Db 491 CTTAGAGCTCTTTTGTGCTTCTGCTTCTGCTTCAAGCACTGATTTTATTTGACACCC 432
OY 754 ACTGAGCTCGGTAACTTGTGAGAAACAGCCGATTCACCTGAGCAGAGACTCTGAAAC 813
Db 431 ACTGAGCTCGGTAACTTGTGAGAAACAGCCGATTCACCTGAGCAGAGACTCTGAAAC 372
OY 814 CTGAGCAGATGTTCTGATGATGCTTACGCTGATGTAACAGCCTGCAACGCTGCC 873
Db 371 CTGAGCAGATGTTCTGATGATGCTTACGCTGATGTAACAGCCTGCAACGCTGCC 313
OY 874 TGGCGGTAAACAGCGCTGCAACGCTGCGCTGTAACAGCGCTGCAACGCTGCTG 933
Db 312 TGGCGGTAAACAGCGCTGCAACGCTGCGCTGTAACAGCGCTGCAACGCTGCTG 253
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OY 934 CCGACAGAGTTTCACTGTCAGCTCAAGAGAAAGCCTTGAAGAGCCCTTATCTGTCTCA 993
Db 252 CCGACAGAGTTTCACTGTCAGCTCAAGAGAAAGCCTTGAAGAGCCCTTATCTGTCTCA 193
OY 994 GGAATCAAGAGCCCTTGTGATGATGTCATATCCGGGAGCGACGAGAGGCGCAGGCGC 1053
Db 192 GGAATCAAGAGCCCTTGTGATGATGTCATATCCGGGAGCGACGAGAGGCGCAGGCGC 133
OY 1054 GCGAGCCCTGTGATGATGAGCCCTCAGAACCCCTTGGCTTCCAGGTGAGAAAGGATAGAG 1113
Db 132 GCGAGCCCTGTGATGATGAGCCCTCAGAACCCCTTGGCTTCCAGGTGAGAAAGGATAGAG 73
OY 1114 GTTGGGTTTCCCTCTTATAGATGTCACGACCTGCGGTGTTACAAAGTTGATGTGG 1172
Db 72 GTTGGGTTTCCCTCTTATAGATGTCACGACCTGCGGTGTTAAAGTTGATGTGG 13
OY 1173 CATGATATCTTT 1184
Db 12 CATGATATMDT 1
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RESULT 2
 AL560722 1023 bp mRNA linear EST 31-MAY-2003
 LOCUS
 DEFINITION
 Homo sapiens cDNA clone CS0DL004YM02 5-PRIME, mRNA sequence.
 ACCESSION
 AL560722
 VERSION
 AL560722.2 GI:31284851
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 1023)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On Feb 15, 2001 this sequence version replaced gi:12907454.
 COMMENT
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 7222.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DL004BG01Q1&cluster=7222.r. Contact :
 Feng Liang Email : fliang@life.techn.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DL004BG01Q1.

FEATURES

source

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/cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
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/clone_11b="Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
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ORIGIN

Query Match 71.9%; Score 952; DB 9; Length 1023;
 Best Local Similarity 98.9%; Pred. No. 1.9e-187;
 Matches 963; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

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OY 8 GGCTGTGCTCTTGTCTTATAGGCGCGCCGAGAGCCGATGCGCGACACTGG 67
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Db      51 GATCTGGCTCTTGGCTTTAGCGCGGCCGAGAGGCCATGCGCGGACCTCG 110
Qy      68 GGGAGGAGTACGACGACCAACCGGACCGCTGTGGGCTGGAGAGTTCCGTATTTGG 127
Db      111 GGGAGGAGTACGACGACCAACCGGACCGCTGTGGGCTGGAGAGTTCCGTATTTGG 170
Qy      128 ACGAGAGCAGACGCGCTGCGCTGACCATGAGATTAAGATAGTTACAGTTAC 187
Db      171 ACGAGAGCAGACGCGCTGCGCTGACCATGAGATTAAGATAGTTACAGTTAC 230
Qy      188 GGGTCTCTTGGCTGGGAGAGCTGCTCTGGGAGGCTATGACCCCAACCCAGATAG 247
Db      221 GGGTCTCTTGGCTGGGAGAGCTGCTCTGGGAGGCTATGACCCCAACCCAGATAG 290
Qy      248 GCCCAAGCTGCTGCTATCATGTGAGCTGCTTACCTGATGAGATACCATCTCTAG 307
Db      291 GCCCAAGCTGCTGCTATCATGTGAGCTGCTTACCTGATGAGATACCATCTCTAG 350
Qy      308 ACTCAGTTTCTGCGCTTATGATACCATGAGATTAAGATAGTTACAGTTAC 367
Db      351 ACTCAGTTTCTGCGCTTATGATACCATGAGATTAAGATAGTTACAGTTAC 410
Qy      368 TCGAGCTGCTGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 427
Db      411 TCGAGCTGCTGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 470
Qy      428 GGGGCTGAGCTGCGCTGACCTTACATGAGGAGATGATGATGATGATGATGATGAT 487
Db      471 GGGGCTGAGCTGCGCTGACCTTACATGAGGAGATGATGATGATGATGATGATGAT 530
Qy      488 ATGCTGTGTCTTCTCCACACGCTGGGCTGAGAGAGATGAGACAGACAGATGAGC 547
Db      531 ATGCTGTGTCTTCTCCACACGCTGGGCTGAGAGAGATGAGACAGACAGATGAGC 590
Qy      548 TCTACCCAGGCTGCGAGACCTGCTGTAGCCCACTGCTGCTGCTGCTGCTGCTGCT 607
Db      591 TCTACCCAGGCTGCGAGACCTGCTGTAGCCCACTGCTGCTGCTGCTGCTGCTGCT 650
Qy      608 CCTGCAAGAGAGATTCATTTGGAGAGCTTCTCCAGAGCTCCAGCTATACCTGTGCC 667
Db      651 CCTGCAAGAGAGATTCATTTGGAGAGCTTCTCCAGAGCTCCAGCTATACCTGTGCC 710
Qy      668 TCGGCTTTCTCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 727
Db      711 TCGGCTTTCTCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 770
Qy      728 GCACTAGTATTCATGTTGACACACCACTCAGCTCCGTGAACCTTGTGAGAACACAGCCGA 787
Db      771 GCACTAGTATTCATGTTGACACACCACTCAGCTCCGTGAACCTTGTGAGAACACAGCCGA 830
Qy      788 TTCACCTGAGACGACCTCTGAAACCTTGTGAGACGATGCTCTACATGTTGCTACGCTTGC 847
Db      831 TTCACCTGAGACGACCTCTGAAACCTTGTGAGACGATGCTCTACATGTTGCTACGCTTGC 890
Qy      848 ATGTAAACAGCGCTGCAAAAGCTGCTGCGGTAAACAGCTGCAAAAGCTGCTGCGC 907
Db      891 ATGTAAACAGCGCTGCAAAAGCTGCTGCGGTAAACAGCTGCAAAAGCTGCTGCGC 949
Qy      908 GTAAACAGCGCTGCAAAAGCTGCTGCGGTAAACAGCTGCAAAAGCTGCTGCGC 967
Db      950 GTAAACAGCGCTGCAAAAGCTGCTGCGGTAAACAGCTGCAAAAGCTGCTGCGC 1009
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Db      1010 CTGAAAGAGAGCCTT 1023

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RESULT 3
LOCUS   BX421512      1201 bp      mRNA      linear      EST 15-MAY-2003
DEFINITION
BX421512 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens cDNA
clone CS00G007YM24 5-PRIME, mRNA sequence.
ACCESSION
BX421512

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VERSION
BX421512.1  GI:30769692
KEYWORDS
EST
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
1 (bases 1 to 1201)
AUTHORS
Li W.B., Gruber C., Jessee J., and Poyas D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished (2001)
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr. Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7413.r
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS00G007BG12QPI.
FEATURES
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1..1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS00G007YM24"
/tissue_type="B CELLS (RAMOS CELL LINE)"
/cell_line="RAMOS CELL LINE"
/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE)"
/notes="vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

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ORIGIN

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Query Match      71.1%; Score 941.4; DB 13; Length 1201;
Best Local Similarity 98.5%; Pred. No. 3e-185;
Matches 976; Conservative 5; Mismatches 6; Indels 4; Gaps 3;

Qy      6 GAGGCTGTGCTCTTCTTCTTGAAGCGGCGGAGAGCCCATGCGCGAGTCCGACACT 65
Db      55 GGGATTCGTGCTCTTCTTCTTGAAGCGGCGGAGAGCCCATGCGCGAGTCCGACACT 114
Qy      66 CGGAGAGCAGTCAACCGACCAACCGGAGCGCTGTGGGCTGGAGAGTTCCGTATATT 125
Db      115 CGGAGAGCAGTCAACCGACCAACCGGAGCGCTGTGGGCTGGAGAGTTCCGTATATT 174
Qy      126 GAGCAGAGAGAGACGCGCTGCTGCTTAAACATCGAGATTAAGATAGGTTACAGTT 185
Db      175 GAGCAGAGAGAGACGCGCTGCTGCTTAAACATCGAGATTAAGATAGGTTACAGTT 234
Qy      186 ACGGCTGCTCTTGGCTGGGAGAGAGTGTCTTGGGAGGAGGCTATGACCCCAACGAGT 245
Db      225 ACGGCTGCTCTTGGCTGGGAGAGAGTGTCTTGGGAGGAGGCTATGACCCCAACGAGT 294
Qy      246 AGGCCCAAGCTGCTGCTATCATGTGAGCTCTTACCTGATGAGACGATACCGATCTTC 305
Db      295 AGGCCCAAGCTGCTGCTATCATGTGAGCTCTTACCTGATGAGACGATACCGATCTTC 354
Qy      306 AGACTCCAGTTTCTGAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 365
Db      355 AGACTCCAGTTTCTGAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 414
Qy      366 TCTGAGCTGCTGCCAGATGACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 425
Db      415 TCTGAGCTGCTGCCAGATGACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 474
Qy      426 CAGGCGCTGAGCTGCGCAGCTCAATGAGGAGATGATGATGATGATGATGATGATGATGAT 485
Db      475 CAGGCGCTGAGCTGCGCAGCTCAATGAGGAGATGATGATGATGATGATGATGATGATGAT 534
Qy      486 CTATGCTGTGTCTTCTCCACACGCTGCGGCTGCGGAGATGAGACAGAGAGATGAG 545

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Db 535 CTATGCTGTGTCTTCTCCACGACGCTGGGGTCTGGAGATGAGACAGAGAGATGA 594
Qy 546 GCTTACACCGAGGCTTGCAGACCTGCTGTAGCCOACTTGTGCTTACCTAGCACTACCA 605
Db 555 GCTTACACCGAGGCTTGCAGACCTGCTGTAGCCOACTTGTGCTTACCTAGCACTACCA 654
Qy 606 CTCCTGCCAAGAGATTCCATTTTGGCAGAGCTTCTCCAGGTGCGCCAGCTATACCTGTG 665
Db 655 CTCCTGCCAAGAGATTCCATTTTGGCAGAGCTTCTCCAGGTGCGCCAGCTATACCTGTG 714
Qy 666 CCTGGGCTTTTCTCAGCTGGATGATGATCTTTCAGCTCTTCTGTCCTTCCCTTCCCTCA 725
Db 715 CTTGGGCTTTTCTCAGCTGGATGATGATGATCTTTCAGCTCTTCTGTCCTTCCCTTCCCTCA 774
Qy 726 CAGCCTGTATTTTATGTTGACACCACTCAGCTCCGTGAACCTTGTGAGAACAGACC 785
Db 775 CAGCCTGTATTTTATGTTGACACCACTCAGCTCCGTGAACCTTGTGAGAACAGACC 834
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Qy 966 GCTGAAAGAGCGCTTATCTGTGCTCAGA 996
Db 1013 GC--TGAAAGAGCGCTTATCTGTGCTCAGM 1041

RESULT 4
LOCUS BM927381 1043 bp mRNA linear EST 12-MAR-2002
DEFINITION AGENCOURT 6704648 NIH_MGC_99 Homo sapiens cdna clone IMAGE:5796796
5', mRNA sequence.
ACCESSION BM927381
VERSION BM927381.1 GI:19377760
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1043)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM2022 row: c column: 05
High quality sequence stop: 755.
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/clone="IMAGE:5796796"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1b="NIH_MGC_99"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned

FEATURES
source

into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH-MGC
Library."

ORIGIN

Query Match 69.6%; Score 921; DB 12; Length 1043;
Best Local Similarity 97.7%; Pred. No. 5,3e-181;
Matches 968; Conservative 0; Mismatches 15; Indels 8; Gaps 3;

Qy 4 GAGAGCTCTGGCTCTTCTTTAAGGCGGCCGAGAGCAGATGCGAGTCCCGACA 63
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Qy 64 CTGGGGGAGGAGTCAACCGGACCGGACCGGCTGTGGGCTTGGGAGAAAGTTCTGTAT 123
Db 61 CTGGGGGAGGAGTCAACCGGACCGGACCGGCTGTGGGCTTGGGAGAAAGTTCTGTAT 120
Qy 124 TTGGACGAGAGAGAGACAGCGCTGCTGCTTAAACATCGAGATTAAGATTAG 183
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Qy 184 TTACGGGTCTCTTGGGTGGGAAAGAGTGTCTTGGGAGGCTTATGACCCCACTCAG 243
Db 181 TTACGGGTCTCTTGGGTGGGAAAGAGTGTCTTGGGAGGCTTATGACCCCACTCAG 240
Qy 244 ATAGGCGCAAGCGCTGCGCTATCATGTGGAGCTTACCTGATGAGATTCGATCC 303
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Qy 304 TCAAGCTCAGATTCTTGGGCTTATGATGATCAATCAATGATGACGCGTGGAGACATG 363
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Qy 364 CTCTCTGAGCTGTGCGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 423
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Qy 424 CCCAGGCGCTGAGCGCTGCGAGCTTACAAATGAGGATGATGATGATGATGATGATGAT 483
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Qy 484 TACTATGCTGTGTCTTCTTCCACAGCTGCGGTCTGGAGAAATGACAGACAGATGAT 543
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Db 536 GAGCTTACCGAGGCGCTGCAAGACCTGCTGTAGCCCACTGCTGCTGCTTACCTAG 595
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QY 904 GCCCGTAAACAGCGCTGCAAAAGCTGCTGCCGACACAGATTACAGTGC-AGCTCAAGGA 962
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Db 896 GCCCGTAAACAGCGCTGGAAGCGTCTGCCCAACACAGATTACAGTGCAGACTCAAGGA 955
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QY 963 AA-CGCTGAAAGAGCGCTTATCTGTGCT 991
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Db 956 AAGGCGCTGGAAGGAGCGCTTATCTGT 986
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RESULT 5
BQ061021
LOCUS BQ061021 1031 bp mRNA linear EST 02-APR-2002
DEFINITION AGENCOURT_6863016 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5920041
5', mRNA sequence.
ACCESSION BQ061021
VERSION BQ061021.1 GI:19884692
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1031)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1CM2083 row: b column: 10
High quality sequence scop: 670.
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/clone="IMAGE:5920041"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_99"
/note="Organ: Lymph; Vector: pOTB7, Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

ORIGIN
Query Match 68.4%; Score 905.4; DB 13; Length 1031;
Best Local Similarity 98.8%; Pred. No. 9.2e-178;
Matches 912; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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QY 267 CATGTGGAGCTCTACCTGATGACATACCATCTCTCAAGCTCTTGGCGCTT 326
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Db 241 CATGTGGAGCTCTACCTGATGACATACCATCTCTCAAGCTCTTGGCGCTT 300
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QY 327 AGTGAACCAATCAAGATTGACGGGTGGAAGACATGCTTCCAGCTGTGCGAGATGA 386
| | | | |
Db 301 AGTGAACCAATCAAGATTGACGGGTGGAAGACATGCTTCCAGCTGTGCGAGATGA 360
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QY 387 CTGATGATGTCTTGGAGACAGCTGTCTCTTCAACCCAGGCGCTAGCGCCAGC 446
| | | | |
Db 361 CTGATGATGTCTTGGAGACAGCTGTCTCTTCAACCCAGGCGCTAGCGCCAGC 420
| | | | |
QY 447 CTACATGGGAGATGTTGTTCTTGTTCACCTTGTTACTATGCTGTGTTCTCCAC 506
| | | | |
Db 421 CTACATGGGAGATGTTGTTCTTGTTCACCTTGTTACTATGCTGTGTTCTCCAC 480
| | | | |
QY 507 CACGCTGGGCTTGGGAGGAATGACAGACAGAGATGAGCTTACCCAGGCGCTGCAG 566
| | | | |
Db 481 CACGCTGGGCTTGGGAGGAATGACAGACAGAGATGAGCTTACCCAGGCGCTGCAG 540
| | | | |
QY 567 ACTGCGCTGTAGCCCACTCTGCTGCTTACACTACCACTCTGCGCAAGAGATTCCA 626
| | | | |
Db 541 ACTGCGCTGTAGCCCACTCTGCTGCTTACACTACCACTCTGCGCAAGAGATTCCA 600
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| | | | |
QY 867 CGCTGCTGCGCGGTAAACAGCGCTGCAAAAGCGCTGCTGCTGCTGCTGCTGCTGCTG 926
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RESULT 6
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5', mRNA sequence.
ACCESSION BQ062796
VERSION BQ062796.1 GI:1988936
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 985)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LNCM2094 row: d column: 21
 High quality sequence stop: 744.
 Location/Qualifiers

FEATURES

source

1..985
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 /note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dt priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCAAGAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 library."

ORIGIN

Query Match 68.2%; Score 903; DB 13; Length 985;
 Best Local Similarity 97.6%; Pred. No. 2.9e-177;

Matches 959; Conservative 0; Mismatches 20; Indels 4; Gaps 4;

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Db 122 TTGACGAGAAAGCAGCAGCGCTGGCTGCTTAAACATCGAGATTAAGATAGTTACAG 181
QY 184 TTACGGGTGCTTGGCTGGGAAAGCGTCTCTGGGAGGCGCTATGACCCCAACCCAG 243
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QY 304 TCAGACTTCAGTTCTGGCGCTTAGTATCAACATCAAGATTGACGCGTGGAGACATG 363
Db 302 TCAGACTTCAGTTCTGGCGCTTAGTATCAACATCAAGATTGACGCGTGGAGACATG 361
QY 364 CTTTTCGAGCTGCTGCCAGATGACTATGATGCTTTGGCAGACCTGTCTCTTTCAC 423
Db 362 CTTTTCGAGCTGCTGCCAGATGACTATGATGCTTTGGCAGACCTGTCTCTTTCAC 421
QY 424 CCCAGGCGCTGAGCTGGGCAAGCTCAATAGGGAGATTTGTGTTCTGTTCACCTTCTG 483
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QY 724 CACAGCACTGATTTTTCATGTTGACACCCACTCAGTCCGTGAACTTGGAGAACACAG 783
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QY 960 GAAAGGCTGAAAGAGCCCTT 982
Db 962 GAAAGGCTGAAAGAGCCCT 984

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RESULT 7
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 LOCUS
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 BQ065603 986 bp mRNA linear EST 02-APR-2002
 AGENCOURT 6875295 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5930157
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 BQ065603.1 GI:19894649
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 986)
 NIH-MGC <http://mgi.mgi.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Lou Staudt
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LNCM2109 row: g column: 22
 High quality sequence stop: 654.
 Location/Qualifiers

FEATURES

source

1..986
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 /clone_lib="NIH MGC 99"
 /note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dt priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCAAGAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 library."

ORIGIN

Query Match 67.2%; Score 889.8; DB 13; Length 986;
 Best Local Similarity 96.8%; Pred. No. 1.6e-174;
 Matches 952; Conservative 0; Mismatches 22; Indels 9; Gaps 4;

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QY 72 GGCACATCCAGCAACCCGAGCCGCTGCGGAGGAGGAGTTCGTATATTGAGACA 131
DB 61 GGCACATCCAGCAACCCGAGCCGCTGCGGAGGAGGAGTTCGTATATTGAGACA 120
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DB 121 GAAGCAGACACGCTGCTGCTTAAACATCAGATTAAGATAGATTACATTACGAGT 180
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DB 241 AAGCCTGCTGCTTATCATGCTGAGTCTTACCTGATGAGACATACCATCTCTGAGCTC 300
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RESULT 8
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VERSION B0061232.1 GI:19885088
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1029)
NIH-MGC http://mhc.nci.nih.gov/.
NATIONAL INSTITUTES OF HEALTH, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
AUTHORS Contact: Robert Strausberg, Ph.D.
TITLE Email: cga@bbs-rtmail.nih.gov
COMMENT Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM2083 row: k column: 24
High quality sequence scop: 728.
Location/Qualifiers
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EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the Laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
ORIGIN
Query Match 67.0%; Score 886.6; DB 13; Length 1029;
Best Local Similarity 97.0%; Pred. No. 7.4e-174;
Matches 947; Conservative 0; Mismatches 20; Indels 9; Gaps 4;
QY 20 TGCCTTTAGGCGGCGCCGAGAGACGCGATGCGCGAGCTCCGACACTCGGGAGGAGCTGA 79
DB 1 TGCCTTTAGGCGGCGCCGAGAGACGCGATGCGCGAGTCCCGACACTCGGGAGGAGCTGA 60
QY 80 CCGACACCCGAGACCGCTGCTGCGGAGGAGGAGTTCGTATTTGAGACGAGAGCAGC 139
DB 61 CCGACACCCGAGACCGCTGCTGCGGAGGAGGAGTTCGTATTTGAGACGAGAGCAGC 120
QY 140 ACGCTGCTGCGCTTAAACATCAGATTAAGAGATGATGATGATGATGATGATGATGATGATG 199
DB 121 ACGCTGCTGCGCTTAAACATCAGATTAAGAGATGATGATGATGATGATGATGATGATGATG 180
QY 200 GTGCGGAGAGAGTGTCTGCGGAGGAGCTTATGAGCCCGACCGAGTAGGAGCCAGCTGAC 259
DB 181 GTGCGGAGAGAGTGTCTGCGGAGGAGCTTATGAGCCCGACCGAGTAGGAGCCAGCTGAC 240
QY 260 TGCCTATATGAGGAGCTTACCTGATGAGACGATACCGATTCCTGACATCTCAATTTCT 319
DB 241 TGCCTATATGAGGAGCTTACCTGATGAGACGATACCGATTCCTGACATCTCAATTTCT 300
QY 320 GCGCTTATGATGATCAATCAAGATTGACGCGGAGGAGAGATGCTTCCAGAGCTGCTGC 379

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Db 301 GCGCTTAAATGACCAATCAATGAGATTGACGCGGTGAGAGACATGCTTCTTCAGAGCTGCTGC 360
 QY 380 CAGATGACTGATGATGATGCTTGTGGACAGACCTGCTCTTTTACCCAGAGGCTGAGCCT 439
 Db 361 CAGATGACTGAT-----GTCTTGGACAGACCTGTCTCTCTTTTACCCAGAGGCTGAGCCT 415
 QY 440 GCGCAGCTCAATGAGGAGTGTGTGTTTCTGTTCACCTTGTGTTTACTATGCTGTGTCT 499
 Db 416 GCGCAGCTCAATGAGGAGTGTGTGTTTCTGTTCACCTTGTGTTTACTATGCTGTGTCT 475
 QY 500 TCTCCACACGCTGGGGGCTGGGAGAGATGACACACAGAGATGAGCTCTTACCCAGAGC 559
 Db 476 TCTCCACACGCTGGGGGCTGGGAGAGATGACACAGAGATGAGCTCTTACCCAGAGC 535
 QY 560 CTGCAAGACCTGCTGTAGCCCACTCTGCTCCCTTGAAGCACTTCCCTGCGCAAGAG 619
 Db 536 CTGCAAGACCTGCTGTAGCCCACTCTGCTCCCTTGAAGCACTTCCCTGCGCAAGAG 595
 QY 620 GATTCCATTGGGACAGCTTCTTCCAGGTGCGCAGCTATACCTGTGCTCGCTTTTCTC 679
 Db 596 GATTCCATTGGGACAGCTTCTTCCAGGTGCGCAGCTATACCTGTGCTCGCTTTTCTC 655
 QY 680 AGCTGATGATGATGCTTTCAGCTCTTCTGTCCTTCTGTCCTTCCCTGACAGCACTGATATT 739
 Db 656 AGCTGATGATGATGCTTTCAGCTCTTCTGTCCTTCTGTCCTTCCCTGACAGCACTGATATT 715
 QY 740 CATGTTGACACACCACTGAGCTCGTGAACCTTGTGAGAACACAGCCGATTCACCTGAGCA 799
 Db 716 CATGTTGACACACCACTGAGCTCGTGAACCTTGTGAGAACACAGCCGATTCACCTGAGCA 775
 QY 800 GGAACCTCGAAACCTTGAACCAAGTGTCTCACATGTGTCTAGGCTGATTTAAACAGC 859
 Db 776 GGAACCTCGAAACCTTGAACCAAGTGTCTCACATGTGTCTAGGCTGATTTAAACAGC 835
 QY 860 CTGCAAGACCTGCTGCGGTAAACACGCTGCAAAAGCTG-CCGTCGCCGTAACACAGCC 918
 Db 836 CTGCAAGACCTGCTGCGGTAAACACGCTGCAAAAGCTG-CCGTCGCCGTAACACAGCC 895
 QY 919 TGCACACGCT-GCCTGCCACACAGGTTACGCTGC-AGCTCAAGAAAGGCTGAAAG 975
 Db 896 TGCACACGCTGCTGCGGTAAACACGCTGCAAAAGCTG-AGCTCAAGAAAGGCTGAAAG 955
 QY 976 AGCCCTTATCTGTCT 991
 Db 956 GAGCCCTTATCTGTCT 971
 RESULT 9 982 bp mRNA linear EST 29-MAR-2002
 B0056675
 LOCUS AGENCOURT_6940585 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5809091
 DEFINITION 5', mRNA sequence.
 ACCESSION B0056675
 VERSION B0056675.1 GI:19816015
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 COMMENT
 TITLE
 JOURNAL
 CONTACT: Robert Strausberg, Ph.D.
 Email: cga@pds-1@mail.nih.gov
 Tissue Procurement: Lou Staudt
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/MLNT at:
 http://image.lnl.gov
 Plate: LCM2054 row: c column: 12

FEATURES High quality sequence stop: 667.
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 /clone="IMAGE:5809091"
 /issue_type="lymphoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_1lb="NIH_MGC_99"
 /note="Organ: lymph; Vector: pORF7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCAAGAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the Laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 Library."
 ORIGIN
 Query Match 66.6%; Score 881.4; DB 13; Length 982;
 Best Local Similarity 96.8%; Pred. No. 8.9e-173;
 Matches 910; Conservative 0; Mismatches 27; Indels 3; Gaps 1;
 166 ATAAAGGATAGTTAGAGTTAAGGAGTTCCTGCGTGGGAAAGACCTGCTCTGGGAGG 225
 Db 43 ATAAAGGATAGTTAGAGTTAAGGAGTTCCTGCGTGGGAAAGACCTGCTCTGGGAGG 102
 QY 226 CCTATGACCCCAACCCAGATAGGCCCCAGCCCTGCTCTATATGAGGAGCTTACCT 285
 Db 103 CCTATGACCCCAACCCAGATAGGCCCCAGCCCTGCTCTATATGAGGAGCTTACCT 162
 QY 286 GATGACGATACCGATCTCAGACTGCTGAGCTTGTGCGCTTATGTTACCATCAAGATT 345
 Db 163 GATGACGATACCGATCTCAGACTGCTGAGCTTGTGCGCTTATGTTACCATCAAGATT 222
 QY 346 GACGCGTGAAGACATGCTTCCGAGCTGCGGACAGATGATGATATGCTTGTGGA 405
 Db 223 GACGCGTGAAGACATGCTTCCGAGCTGCGGACAGATGATGATATGCTTGTGGA 282
 QY 406 GCACTGTCTCTTTACCCAGAGGCTGAGCTGCGGACCACTCAATAGGAGATTGTG 465
 Db 283 GCACTGTCTCTTTACCCAGAGGCTGAGCTGCGGACCACTCAATAGGAGATTGTG 342
 QY 466 TTTCTGTTACCTTGTGTTTACTATGCTGTGTCTTCTCACCAGCTGGGATCTGGAGG 525
 Db 343 TTTCTGTTACCTTGTGTTTACTATGCTGTGTCTTCTCACCAGCTGGGATCTGGAGG 402
 QY 526 AATGACAGACAGAGATGAGCTTACCCAGAGGCTGACAGGACCTGCTGAGCCACTC 585
 Db 403 AATGACAGACAGAGATGAGCTTACCCAGAGGCTGACAGGACCTGCTGAGCCACTC 462
 QY 586 TCGTGCCTTACCACTACCACTCTGCGCAAGAGATTCAATTGGACAGACTTCTTCA 645
 Db 463 TCGTGCCTTACCACTACCACTCTGCGCAAGAGATTCAATTGGACAGACTTCTTCA 522
 QY 646 GGTGCGCAGCTATACCTGCGCTGCTTCTGAGCTGATGATGCTTCAAGCTTCTT 705
 Db 523 GGTGCGCAGCTATACCTGCGCTGCTTCTGAGCTGATGATGCTTCAAGCTTCTT 582
 QY 706 TCTGTCCCTTGTGCTTACAGCAGCTAGTATTTTCAATTTGACACACCACTCAGCTCGT 765
 Db 583 TCTGTCCCTTGTGCTTACAGCAGCTAGTATTTTCAATTTGACACACCACTCAGCTCGT 642
 QY 766 GAACTTGTGAACAACAGCCCACTTACCTGACAGACCTTGAACCTTGAACCAAGTGG 825
 Db 643 GAACTTGTGAACAACAGCCCACTTACCTGACAGACCTTGAACCTTGAACCAAGTGG 702
 QY 826 TCTCATATGTTGTTACGCTGATGATTAACACAGCTGCAACGCTGCTGCGGTTAACA 885
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QY 886 CGCCTGCAAAACGCTGCTGCCCCGTAAGACGCGCTGCAAAAGCTGCTGCCCCACAGAGTT 945
DB 763 CGCCTGCAAAAGCTGCTGCCCCGTAAGACGCGCTGCAAAAGCTGCTGCCCCACAGAGTT 822
QY 946 CACGTGCAAGCTTCAAGGAAAGGCTTGAAGAGAGCCCTTATCTGTGCTTCAAGACTCAAGAAC 1005
DB 823 CACGTGCAAGCTTCAAGGAAAGGCTTGAAGAGAGCCCTTATCTGTGCTTCAAGACTCAANAAAC 882
QY 1006 CTCCTGGGTCAGTGTGTCACATCCCGGAGACGAGAGAGGCGACCGGCGGAGCCCTT 1062
DB 883 CTCCTGGGTCAGTGTGTCACATCCCGGAGACGAGAGAGGCGACCGGCGGAGCCCTTGT 942
QY 1063 GTGATGAGACCCCTCAGAACCCCTTGTGCTGCCCCAGCTGGA 1102
DB 943 GGGATGAGCCCTTCGAAACCTTGGGCTGGCCAGCTGTA 982

RESULT 10
LOCUS BG754764 964 bp mRNA linear EST 15-MAY-2001
DEFINITION 60271435P1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4854513 5',
mRNA sequence.
ACCESSION BG754764 GI:14065417
VERSION BG754764.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 964)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbe-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ULNL at:
http://image.llnl.gov
Plate: ILCM1702 row: e column: 10
High quality sequence stop: 886.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4854513"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_1lb="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN
Query Match 66.3%; Score 877.8; DB 12; Length 964;
Best Local Similarity 96.9%; Pred. No. 5e-172;
Matches 927; Conservative 0; Mismatches 27; Indels 3; Gaps 3;

QY 1 CTGTAGAGGCTCTGCTCTTGTCTTTAGGCGGCCCGGAGAGCCATAGCCGAGTGCCTCG 60
DB 3 CTTGAGAGGCTCTGCTCTTGTCTTTAGGCGGCCCGGAGAGCCATAGCCGAGTGCCTCG 62
QY 61 ACACCTGGGAGGAGTACGACGACACCGGAGCGCTGTGGGCTGTGGAGAGATTGCTG 120

DB 63 ACACCTGGGAGGAGTACGACGACACCGGAGCGCTGTGGGCTGTGGAGAGATTGCTG 122
QY 121 TATTTGGAGGAGAGACGACGAGCTGCTGCTTAAACATGAGATTAAGATAGTTA 180
DB 123 TATTTGGAGGAGAGACGACGAGCTGCTGCTTAAACATGAGATTAAGATAGTTA 182
QY 181 CAGTTAGGGGAGTCTTGTGCTGGGAGAGAGTGTGCTGGGAGGCTATAGCCCCACC 240
DB 183 CAGTTAGGGGAGTCTTGTGCTGGGAGAGAGTGTGCTGGGAGGCTATAGCCCCACC 242
QY 241 CAGATAGGCGCCAGAGCTGCTGCTTATCATGTGTGAGCTCTACCTCATAGTGAAGATACGA 300
DB 243 CAGATAGGCGCCAGAGCTGCTGCTTATCATGTGTGAGCTCTACCTCATAGTGAAGATACGA 302
QY 301 TCTCTAGACTCAGTTTCTGGGCTTATGTAACATGAGATTAAGATTAAGATTAAGATTA 360
DB 303 TCTCTAGACTCAGTTTCTGGGCTTATGTAACATGAGATTAAGATTAAGATTAAGATTA 362
QY 361 ATGCTTCTGAGAGCTGCTGCTGAGATGATGATGATGATGATGATGATGATGATGATGATG 420
DB 363 ATGCTTCTGAGAGCTGCTGCTGAGATGATGATGATGATGATGATGATGATGATGATGATG 422
QY 421 CACCCAGAGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 423 CACCCAGAGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 482
QY 481 GTTTATCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
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DB 543 GATGAGCTCTACGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 602
QY 601 TACCACTCTCTGCAAGAGAGATTCATTTGGCAGAGCTTCTTCCAGTGGCCAGCTATAC 660
DB 603 TACCACTCTCTGCAAGAGAGATTCATTTGGCAGAGCTTCTTCCAGTGGCCAGCTATAC 662
QY 661 CTGTGCTGCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
DB 663 CTGTGCTGCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 722
QY 721 CCTCAGCACTATGATTTTATGTTGACACCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
DB 723 CCTCAGCACTATGATTTTATGTTGACACCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 782
QY 781 CAGCGATTTACCTGAGCA-GGACCTGGAACCTGAGCAGTGTCTCA-CATGCTGC 838
DB 783 CAGCGATTTACCTGAGCAGGAGACCTTGAACCTGAGCAGTGTCTCA-CATGCTGC 842
QY 839 T-ACGCTGCTGATTAACACGCTGCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 897
DB 843 TAAAGCTGCTGATTAACACGCTGCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 902
QY 898 CTG 954
DB 903 CTG 959

RESULT 11
LOCUS BM927621 1056 bp mRNA linear EST 12-MAR-2002
DEFINITION AGENTCOURT 6704661 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5797060
5', mRNA sequence.
ACCESSION BM927621
VERSION BM927621.1 GI:19378000
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1056)

II RT (Life Technologies). Note: this is a NIH_MGC Library."

Query Match 65.7%; Score 870.4; DB 13; Length 988;
Best Local Similarity 96.6%; Pred. No. 1.7e-170;
Matches 901; Conservative 0; Mismatches 27; Indels 5; Gaps 1;

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QY 14 GGCCTTGTCTTTAGGCGCCCGAGAGCCGATGCGCCGACACTCGGGAGG 73
DB 1 GGCCTTGTCTTTAGGCGCCCGAGAGCCGATGCGCCGACACTCGGGAGG 60
QY 74 CAGTACCGACACCCGACCGCTGTGGGCTGGGAGAGATTCTGTATTGACGAGA 133
DB 61 CAGTACCGACACCCGACCGCTGTGGGCTGGGAGAGATTCTGTATTGACGAGA 120
QY 134 AGCAGACGCGCTGCTGCTTTAACCATGAGATAAGAGATTACAGTTACGGGTGC 193
DB 121 AGCAGACGCGCTGCTGCTTTAACCATGAGATAAGAGATTACAGTTACGGGTGC 180
QY 194 TCTTGCGTGGGAGAAAGCTGCTGCTGGGAGGCTTATGACCCCGACCGAGATGGCCAA 253
DB 181 TCTTGCGTGGGAGAAAGCTGCTGCTGGGAGGCTTATGACCCCGACCGAGATGGCCAA 240
QY 254 GCCTGCTGCTTATCATGTGGCAGCTCTACCTGATGAGAGATACCGATCTGAGACTCA 313
DB 241 GCCTGCTGCTTATCATGTGGCAGCTCTACCTGATGAGAGATACCGATCTGAGACTCA 300
QY 314 GTTTCGCGCTTATGATGACCATCAAGATTGACGGCGGTGAGAGACATGCTTCGAGC 373
DB 301 GTTTCGCGCTTATGATGACCATCAAGATTGACGGCGGTGAGAGACATGCTTCGAGC 360
QY 374 TGTGCGCGAGTACATGATGATGCTTGGGAGACCTGTCTTCCATCCCGAGGGCT 433
DB 361 TGTGCGCGAGTACATGATGATGCTTGGGAGACCTGTCTTCCATCCCGAGGGCT 415
QY 434 GAGCTGCGACGCTTACATGAGGAGATGTTGTTCTGTTCACCTTCCTTACTATGCT 493
DB 416 GAGCTGCGACGCTTACATGAGGAGATGTTGTTCTGTTCACCTTCCTTACTATGCT 475
QY 494 GTGTCTTTCACACACGCTGGGGTCTGGGAGAGATGAGACAGAGAGATGAGCTTAC 553
DB 476 GTGTCTTTCACACACGCTGGGGTCTGGGAGAGATGAGACAGAGATGAGCTTAC 535
QY 554 CAGGGCTGCGAGAGACTGCTGTAGCCCACTGTCTGCTTACGACTTACCTCTGCC 613
DB 536 CAGGGCTGCGAGAGACTGCTGTAGCCCACTGTCTGCTTACGACTTACCTCTGCC 595
QY 614 AAGGAGATTCATTTGGCAGAGCTTCTCCAGTGGCCAGCTATACCTGTCGGCT 673
DB 596 AAGGAGATTCATTTGGCAGAGCTTCTCCAGTGGCCAGCTATACCTGTCGGCT 655
QY 674 TTTCTCAGCTGATGATGATCTTTCAGCCCTTTCTGTCTCTGTCCTCAGACAGTA 733
DB 656 TTTCTCAGCTGATGATGATCTTTCAGCCCTTTCTGTCTCTGTCCTCAGACAGTA 715
QY 734 GTATTTCATGTTGACACACCACTACGCTCCGTAACCTTGTAAGAACACAGCCGATTCAC 793
DB 716 GTATTTCATGTTGACACACCACTACGCTCCGTAACCTTGTAAGAACACAGCCGATTCAC 775
QY 794 TGAGCAGAGACCTCTGAAACCCGAGCAAGTGCTCAGATGGTGTACGGCTGAGTTAA 853
DB 776 TGAGCAGAGACCTCTGAAACCCGAGCAAGTGCTCAGATGGTGTACGGCTGAGTTAA 835
QY 854 ACAGCCTGCAAAACGCTGCTGCGGTAAACAGCCTGCAAAACGCTGCTGCGGTAAAC 913
DB 836 ACAGCCTGCAAAACGCTGCTGCGGTAAACAGCCTGCAAAACGCTGCTGCGGTAAAC 895
QY 914 ACGCTGCAAAACGCTGCTGCGGTAAACAGCCTGCAAAACGCTGCTGCGGTAAAC 946
DB 896 ACGCTGCAAAACGCTGCTGCGGTAAACAGCCTGCAAAACGCTGCTGCGGTAAAC 928

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RESULT 13

B0059785

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

B0059785 990 bp mRNA linear EST 29-MAR-2002
AGENCOURT 6739989 NIH_MGC_99 Homo sapiens CDNA clone IMAGE:5815893
5', mRNA sequence.

B0059785
B0059785.1 GI:19819125

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 990)

NIH-MGC <http://mgc.nci.nih.gov/>

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Lou Staudt

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

<http://image.lnl.gov>

Plate: LNCM2071 row: n column: 22

High quality sequence stop: 746.

Location/Qualifiers

1. 990

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/tissue_type="lymphoma, cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH MGC 99"

/note="Organ: lymph; Vector: pOT87; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dt priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GGGACGAG(G). Size-selected >500bp for average insert size

1.8kb. Library constructed by Ling Hong in the laboratory

of Gerald M. Rubin (University of California, Berkeley)

using ZAP-cDNA synthesis kit (Stratagene) and Superscript

II RT (Life Technologies). Note: this is a NIH_MGC

Library."

ORIGIN

Query Match 64.8%; Score 858.2; DB 13; Length 990;

Best Local Similarity 99.4%; Pred. No. 5.9e-168;

Matches 882; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

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QY 5 AGAGGCTGTGCTCTTCTTATGAGCGCCGAGAGCGCCATGCGAGTCCGACAC 64
DB 1 AGAGGCTGTGCTCTTCTTATGAGCGCCGAGAGCGCCATGCGAGTCCGACAC 60
QY 65 TCGGGAGGAGTACCGACCAACCCGACCGCTGTGGGCTTGGGAGAAATTCTGTATT 124
DB 61 TCGGGAGGAGTACCGACCAACCCGACCGCTGTGGGCTTGGGAGAAATTCTGTATT 120
QY 125 TGAGCAGAGACGACGACGCTGCTGCTTAAACATGAGATAAGAGATTACAGT 184
DB 121 TGAGCAGAGACGACGACGCTGCTGCTTAAACATGAGATAAGAGATTACAGT 180
QY 185 TAGGGGTGCTTCTGCTGGGAGAGCGTGTCTTGGGAGGCTTATGACCCCGACCA 244
DB 181 TAGGGGTGCTTCTGCTGGGAGAGCGTGTCTTGGGAGGCTTATGACCCCGACCA 240
QY 245 TAGGCGCAAGCCTGCTTATCATGTGGCAGCTCTACCTGATGAGAGATACGATCT 304
DB 241 TAGGCGCAAGCCTGCTTATCATGTGGCAGCTCTACCTGATGAGAGATACGATCT 300
QY 305 CAGACTCAGATTCTGCGGCTTATGATGACCATCAAGATTGAGGCGCTGAGGACATGC 364

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Db      301 CAGACTCCAGTTTCTGGCGCTTAGTGTACACATCAAGATTGACGGCGTGGAGACATGC 360
Qy      365 TTCTGAGCTGCTGGCCAGATGA CTGATGTATGCTTTGGCAGACCTGCTCTTCCACC 424
Db      361 TTCTGAGCTGCTGGCCAGATGA CTGATGTATGCTTTGGCAGACCTGCTCTTCCACC 420
Qy      425 CCAGGGCTTGAAGCTTGGCCAGCTTACATAGGGAGATGTTGTCTTGTTCATCTTCGTTT 484
Db      421 CCAGGGCTTGAAGCTTGGCCAGCTTACATAGGGAGATGTTGTCTTGTTCATCTTCGTTT 480
Qy      485 ACTATGCGCTGCTGCTTCTCCACACAGCTGGGGCTTGGAGAGATGACAGACAGAGATG 544
Db      481 ACTATGCGCTGCTGCTTCTCCACACAGCTGGGGCTTGGAGAGATGACAGAGAGATG 540
Qy      545 AGCTTACCCAGAGGGCTTGGAGAGACTGCTTGAAGCCACTGCTGCGCTTAGACTATACC 604
Db      541 AGCTTACCCAGAGGGCTTGGAGAGACTGCTTGAAGCCACTGCTGCGCTTAGACTATACC 600
Qy      605 ACTCTGCCAGAGAGATTCATTTTGGCAGAGCTTCTTCCAGATGCCAGCTATACCTGT 664
Db      601 ACTCTGCCAGAGAGATTCATTTTGGCAGAGCTTCTTCCAGATGCCAGCTATACCTGT 660
Qy      665 GCTTGGCTTTTCTGAGCTGAGATGATGCTTTCAGGCTCTTCTGCTCTTCTGCTCTC 724
Db      661 GCTTGGCTTTTCTGAGCTGAGATGATGCTTTCAGGCTCTTCTGCTCTTCTGCTCTC 720
Qy      725 ACAGCACTAGTATTTTCACTGTTGACACACCCACTGAGCTCGTGAACCTTGTGAGAACACAGC 784
Db      721 ACAGCACTAGTATTTTCACTGTTGACACACCCACTGAGCTCGTGAACCTTGTGAGAACACAGC 780
Qy      785 CGATTCACTGAGAGAGACTTGTGAACCTTGGACCAAGTGTCTTCACTGTTGAGTACGCC 844
Db      781 CGATTCACTGAGAGAGACTTGTGAACCTTGGACCAAGTGTCTTCACTGTTGAGTACGCC 840
Qy      845 TGCATGTAAACAGC- CCTGCAACAGCTG- CCTGCGGTAACAGGCC 889
Db      841 TGCATGTAAACAGCCTGCAACAGCTGCTGCGGTAACAGCCCC 887

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RESULT 14
LOCUS   BM927418
DEFINITION 1024 bp mRNA linear EST 12-MAR-2002
AGENCOURT_6704874 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5796834
VERSION BM927418
KEYWORDS BM927418.1 GI:19377797
SOURCE  EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1024)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: gsa@broad.mit.edu
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM2022 row: d column: 19
High quality sequence stop: 746.
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5796834"
/tissue_type="lymphoma, cell line"

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FEATURES

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/organism="Homo sapiens"
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ORIGIN

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Query Match 64.8%; Score 858.2; DB 12; Length 1024;
Best Local Similarity 98.8%; Pred. No. 5.9e-168;
Matches 874; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

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/lab host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_99"
/note="Organ: lymph; Vector: pOT7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
library."

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 5', mRNA sequence.

ACCESSION BM927384.1 GI:19377763
 VERSION BM927384
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 TITLE NIH-MGC http://mgi.nci.nih.gov/
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Lou Staudt
 CDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: Agencourt Bioscience Corporation (LNL)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
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FEATURES
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 into EcoRI/XhoI sites using the following 5' adaptor:
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 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-CDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 library."

ORIGIN

Query Match 64.7%; Score 856.6; DB 12; Length 1038;
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 Matches 910; Conservative 0; Mismatches 9; Indels 8; Gaps 4;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Searched: 682709 seqs, 277475446 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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2	1324	100.0	1324	5	PCT-US95-1363-1 Sequence 1, Appli
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4	819.8	61.9	4922	2	US-08-330-272-5 Sequence 5, Appli
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ALIGNMENTS

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US-08-330-272-1
Sequence 1, Application US/08330272
Patent No. 5985598
GENERAL INFORMATION:
APPLICANT: Russo et al
TITLE OF INVENTION: TGL-1 Gene and Protein and Related
TITLE OF INVENTION: Methods and Compositions
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/330,272
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6754-027
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 790-8664/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1324 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 49..387
US-08-330-272-1
Query Match 100.0%; Score 1324; DB 2; Length 1324;
Best local similarity 100.0%; Pred. No. 0;
Matches 1324; Conservative 0; Indels 0; Gaps 0;
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Qy	1321	AAAA	1324
Db	1321	AAAA	1324

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RESULT 2
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; GENERAL INFORMATION:
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; TITLE OF INVENTION: TcI-1 Gene and Protein and Related
; TITLE OF INVENTION: Methods and Compositions
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13663
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6754-027
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 790-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1324 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
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; LOCATION: 49..387
; PCT-US95-13663-1

Query Match 100.0%; Score 1324; DB 5; Length 1324;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1324; Conservative 0; Indels 0; Gaps 0

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Db 961 GAAAGGCTGAAAGAGGCTTATCTGTGCTCAGAGCTCAGAAAGCTCTGGGTCAAGTGT 1020
QY 1021 CCACTATCCCGGAGAGCAGAGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 1080
Db 1021 CCACTATCCCGGAGAGCAGAGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 1080
QY 1081 CCGTGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 1140
Db 1081 CCGTGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 1140
QY 1141 CACGCACTGGGTGTATCAAAAGTGTATGTGAGCATGAATACCTTTTGTATGATGATTA 1200
Db 1141 CACGCACTGGGTGTATCAAAAGTGTATGTGAGCATGAATACCTTTTGTATGATGATTA 1200

QY 1201 AATGCAAGATAGTTATCTTAACCTTGGAGGCAATCAGCTTCTATCTTGAATTAATCT 1260
Db 1201 AATGCAAGATAGTTATCTTAACCTTGGAGGCAATCAGCTTCTATCTTGAATTAATCT 1260
QY 1261 GGTGAGAGAAATGAGAAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
Db 1261 GGTGAGAGAAATGAGAAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
QY 1321 AAAA 1324
Db 1321 AAAA 1324

RESULT 3
US-09-620-312D-871
; Sequence 871, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyen
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yundong
; APPLICANT: Wang, Duntui
; APPLICANT: Wang, Zhwei
; APPLICANT: John Tillingshast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620, 312D
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552, 317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488, 725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pc FL_genes Version 1.0
; SEQ ID NO 871
; LENGTH: 1368
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (103)..(447)
US-09-620-312D-871

Query Match 96.7%; Score 1280; DB 4; Length 1368;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1302; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 8 GGCCTGGCTCTGCTTCTTATGAGGCGCCGAGAGAGCAGATGAGCGGAGCACTCG 67
Db 65 GGCCTGGCTCTGCTTCTTATGAGGCGCCGAGAGAGCAGATGAGCGGAGCACTCG 124
QY 68 GGGAGGAGTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 127
Db 125 GGGAGGAGTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 184
QY 128 ACGAAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 187
Db 185 ACGAAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 244
QY 188 GGGGTCTTGTGCTGAGGAGAGCGTGTCTGAGGAGGCTATGACCCCAACGATGAG 247


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OY 754 ACTCAGCTCCGTGAACCTTGTGAGAACACAGCCGATTCCTGAGCAGACCTCTGAAACC 813
DB 4086 ACTCAGCTCCGTGAACCTTGTGAGAACACAGCCGATTCCTGAGCAGACCTCTGAAACC 4145
OY 814 CTGACACAGTGTGTCACTGTGTGCTACGCTGTGATGTAACAGCCTTGCAACGCTGCG 873
DB 4146 CTGACACAGTGTGTCACTGTGTGCTACGCTGTGATGTAACAGCCTTGCAACGCTGCG 4205
OY 874 TGCCCGTAAACACGCTGTGAAC-C-GTGTCTCCCGTAAACAGCCTTGCAACGCTGCGT 932
DB 4206 TGCCCGTAAACACGCTGTGAAC-C-GTGTCTCCCGTAAACAGCCTTGCAACGCTGCGT 4265
OY 933 GCCCAGCAGGTTCACTGTGCTGCTCAGAGAAAGCCGTGAAGAGCCCTTATCTGTGCTC 992
DB 4266 GCCCAGCAGGTTCACTGTGCTGCTCAGAGAAAGCCGTGAAGAGCCCTTATCTGTGCTC 4325
OY 993 AGGACTCAGAAAGCCTCTGTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1052
DB 4326 AGGACTCAGAAAGCCTCTGTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4385
OY 1053 GCGGAGCCCTGTGTGATGAGCCCTCAGAACCTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1112
DB 4386 GCGGAGCCCTGTGTGATGAGCCCTCAGAACCTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4445
OY 1113 GGTGGGTTTCCCGCC-TTTATAGATGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1171
DB 4446 GGTGGGTTTCCCGCC-TTTATAGATGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 4505
OY 1172 GCATGAATACCTTTTGTATGATGATTAATATGCAAGATGTTATCTAACTTGTGCGC 1231
DB 4506 GCATGAATACCTTTTGTATGATGATTAATATGCAAGATGTTATCTAACTTGTGCGC 4565
OY 1232 AATCAGCTTCTATCTCTGACTTAAGATTCGTGTGAGAGAGAGTGAATAGGAGCCCA 1291
DB 4566 AATCAGCTTCTATCTCTGACTTAAGATTCGTGTGAGAGAGTGAATAGGAGCCCA 4625
OY 1292 AATAAATAATTCATGGA 1311
DB 4626 AATAAATAATTCATGGA 4645

```

```

RESULT 5
PCT-US95-13663-5
Sequence 5, Application PC/TUS9513663
GENERAL INFORMATION:
APPLICANT: Russo et al
TITLE OF INVENTION: TGL-1 Gene and Protein and Related
NUMBER OF INVENTION: Methods and Compositions
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13663
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6754-027
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 790-8864/9741
TELEX: 66141 PENNIE

```

```

; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4922 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
PCT-US95-13663-5

```

```

Query Match 61.9%; Score 819.8; DB 5; Length 4922;
Best Local Similarity 92.8%; Pred. No. 2.8e-248;
Matches 854; Conservative 28; Mismatches 34; Indels 4; Gaps 4;

```

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OY 396 GGTCTTGACACACCTGCTCTCTTACCCAGAGGCTGAGCTTGGCCAGCTTAAGATGG 455
DB 3726 GGTCTTGACACACCTGCTCTCTTACCCAGAGGCTGAGCTTGGCCAGCTTAAGATGG 3785
OY 456 GATGTGTGTGTTCTGTTCACTGTTTAACTATGCTGTGCTTCTCAGCAGCCTGGG 515
DB 3786 GATGTGTGTGTTCTGTTCACTGTTTAACTATGCTGTGCTTCTCAGCAGCCTGGG 3845
OY 516 GTCTGGAGAAATGACACAGACAGATGAGCTTACCCAGGCTGACAGACCTG-CTT 574
DB 3846 GTCTGGAGAAATGACACAGACAGATGAGCTTACCCAGGCTGACAGACCTGCTCCT 3905
OY 575 GTAGCCCACTGCTGCTGCTTACCA-CTACACCTCTGACCAAGAGGATTCATTGGCA 633
DB 3906 GTAGCCCACTGCTGCTGCTTACCA-CTACACCTCTGACCAAGAGGATTCATTGGCA 3965
OY 634 GAGCTTCTTCCAGAGTGCCTATACCTGTGCTGCTGCTTCTCAGCTGATGATGT 693
DB 3966 GAGCTTCTTCCAGAGTGCCTATACCTGTGCTGCTGCTTCTCAGCTGATGATGT 4025
OY 694 CTTCAGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 753
DB 4026 CTTCAGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4085
OY 754 ACTCAGCTCCGTGAACCTTGTGAGAACACAGCCGATTCCTGAGCAGACCTCTGAAACC 813
DB 4086 ACTCAGCTCCGTGAACCTTGTGAGAACACAGCCGATTCCTGAGCAGACCTCTGAAACC 4145
OY 814 CTGACACAGTGTGTCACTGTGTGCTACGCTGTGATGTAACAGCCTTGCAACGCTGCG 873
DB 4146 CTGACACAGTGTGTCACTGTGTGCTACGCTGTGATGTAACAGCCTTGCAACGCTGCG 4205
OY 874 TGCCGTAAACACGCTGTGAAC-C-GTGTCTCCCGTAAACAGCCTTGCAACGCTGCGT 932
DB 4206 TGCCGTAAACACGCTGTGAAC-C-GTGTCTCCCGTAAACAGCCTTGCAACGCTGCGT 4265
OY 933 GCCCAGCAGGTTCACTGTGCTGCTCAGAGAAAGCCGTGAAGAGCCCTTATCTGTGCTC 992
DB 4266 GCCCAGCAGGTTCACTGTGCTGCTCAGAGAAAGCCGTGAAGAGCCCTTATCTGTGCTC 4325
OY 993 AGGACTCAGAAAGCCTCTGTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1052
DB 4326 AGGACTCAGAAAGCCTCTGTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4385
OY 1053 GCGGAGCCCTGTGTGATGAGCCCTCAGAACCTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1112
DB 4386 GCGGAGCCCTGTGTGATGAGCCCTCAGAACCTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4445
OY 1113 GGTGGGTTTCCCGCC-TTTATAGATGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1171
DB 4446 GGTGGGTTTCCCGCC-TTTATAGATGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 4505
OY 1172 GCATGAATACCTTTTGTATGATGATTAATATGCAAGATGTTATCTAACTTGTGCGC 1231
DB 4506 GCATGAATACCTTTTGTATGATGATTAATATGCAAGATGTTATCTAACTTGTGCGC 4565
OY 1232 AATCAGCTTCTATCTCTGACTTAAGATTCGTGTGAGAGAGTGAATAGGAGCCCA 1291
DB 4566 AATCAGCTTCTATCTCTGACTTAAGATTCGTGTGAGAGAGTGAATAGGAGCCCA 4625

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QY 1292 AATAAATAATTCATGGAA 1311
|||||
Db 4626 NATAAANATATTCANGGGA 4645

RESULT 6

US-08-330-272-3
Sequence 3, Application US/08330272
Patent No. 5985598
GENERAL INFORMATION:
APPLICANT: Russo et al
TITLE OF INVENTION: TCL-1 Gene and Protein and Related
TITLE OF INVENTION: Methods and Compositions
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/330,272
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6754-027
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 790-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 560 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-330-272-3

Query Match 4.9%; Score 65; DB 2; Length 560;
Best Local Similarity 100.0%; Pred. No. 2.5e-10;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGAGAGGCTCTGGCTCTTGTCTTAGGCGGCCGAGAGCGCCATGGCCGAGTGCCCG 60
|||||
Db 496 CTTGAGAGGCTCTGGCTCTTGTCTTAGGCGGCCGAGAGCGCCATGGCCGAGTGCCCG 555

QY 61 AACT 65
|||||
Db 556 AACT 560

RESULT 7

PCT-US95-13663-3
Sequence 3, Application PC/TUS9513663
GENERAL INFORMATION:
APPLICANT: Russo et al
TITLE OF INVENTION: TCL-1 Gene and Protein and Related
TITLE OF INVENTION: Methods and Compositions
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York

COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13663
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6754-027
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 790-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 560 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
PCT-US95-13663-3

Query Match 4.9%; Score 65; DB 5; Length 560;
Best Local Similarity 100.0%; Pred. No. 2.5e-10;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGAGAGGCTCTGGCTCTTGTCTTAGGCGGCCGAGAGCGCCATGGCCGAGTGCCCG 60
|||||
Db 496 CTTGAGAGGCTCTGGCTCTTGTCTTAGGCGGCCGAGAGCGCCATGGCCGAGTGCCCG 555

QY 61 AACT 65
|||||
Db 556 AACT 560

RESULT 8

US-08-232-463-14
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:

```

; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: PT59pt-F18
; US-08-232-463-14

Query Match          3.7%; Score 49.2; DB 1; Length 7218;
Best Local Similarity 2.3%; Pred.No.0.00013;
Matches 9; Conservative 221; Mismatches 154; Indels 0; Gaps 0;

QY 399 CTGGCAGCAGCTGCTCTCTTACCCAGGCGCTGAGCTGGCCAGCTTACATGGGGA 458
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1059 CTGGCAGATYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1118
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 459 TGTGTGTTTCTGTCACCTTGTTTACTATGCTGTGCTTCTGCACACGCTGGGTC 518
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1119 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1178
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 519 TGGGAGATGAGACAGACAGAGATGAGCTTACCCAGGCGCTGAGAGCTGCTGTAG 578
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1179 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1238
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 579 CCCACTGCTGCTGCTTACACTACACTCCTGCCAAGAGAGATTCATTGGCAGAGCT 638
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1239 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1298
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 639 TCTTCAGAGTGCAGCTATACCTGCTGCTGCTTTCTCTACGCTGAGTGAAGTCTTCA 698
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1299 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1358
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 699 GCCTCTTCTGCTCTGCTGCTGCTCAGACAGCACTAGTATGATGTGCACACCCACTCA 758
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1359 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1418
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 759 GCTCCGTGAAGCTGTGAGAACACA 782
    : : : : : : : : : : | | | |
DB 1419 YYYYYYYYYYYYYYGTACCAAA 1442
    : : : : : : : : : : | | | |

RESULT 9
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
```

```

; OTHER INFORMATION: represent a, t, c or g
; US-09-103-840A-2

Query Match          3.2%; Score 41.8; DB 3; Length 4403765;
Best Local Similarity 53.3%; Pred.No.1.6;
Matches 88; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 3 TGAGAGGCTGAGCTGCTTCTTTTAAAGGCGGCGGAGAGCGCATGGCGAGTCCGAC 62
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 2356523 TGCGGCTGTATCTCATCGAGTGGGCAATCCGAGTACCGCACCGCGAATGGACAG 2356464
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 63 ACTCGGAGGAGCAGTCAACCAACACCCGAGCGCTGTGGGCTTGGGAGAAATTGCTGTA 122
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 2356463 CCTGTGACGTGTGTACCACTGACCGGGCGGTGAATGGGTGTGGAAGACTGCTCGT 2356404
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 123 TTGGAGCAGAAAGCAGCAGCGCTGCTGCTTAACTTCAAGAT 167
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 2356403 TGACGCCAGAGCAGCGGCTGCGCAGAGAGGAGATGCGCGGCAGCAT 2356359
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
US-09-007-005-17/c
; Sequence 17, Application US/09007005B
; Patent No. 6258558
; GENERAL INFORMATION:
; APPLICANT: Szoestak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihue
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; FILE REFERENCE: 00786/350003
; CURRENT APPLICATION NUMBER: US/09/007,005B
; CURRENT FILING DATE: 1998-01-14
```

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RESULT 12
US-09-244-796-17/c
/ Sequence 17, Application US/09244796
/ Patent No. 6281344
/ GENERAL INFORMATION:
/ APPLICANT: Szoestak, Jack W.
/ APPLICANT: Roberts, Richard W.
/ APPLICANT: Liu, Rihue
/ TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
/ TITLE OF INVENTION: FUSIONS
/ FILE REFERENCE: 00786/350007
/ CURRENT APPLICATION NUMBER: US/09/244,796
/ CURRENT FILING DATE: 1999-02-05
/ EARLIER APPLICATION NUMBER: 60/035,963
/ EARLIER FILING DATE: 1997-01-27
/ EARLIER APPLICATION NUMBER: 60/064,491
/ EARLIER FILING DATE: 1997-11-06
/ EARLIER APPLICATION NUMBER: 09/007,005
/ EARLIER FILING DATE: 1998-01-14
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 17
/ LENGTH: 289
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Translation template
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)...(289)

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QY	567	ACCGGCGCTTGAAGCCACCTGCTGGGCTTGA	CTACACACTCGTGGCAGAGAGATTCCA	626
Db	586	ACCGGCGCCAAAGCTGCTCCACCCCGAGCC	ACCAGCCCGAGCCCGACGACGACAACT	527
QY	627	TTTGGCAGAGCTTCTTCAGAGTGCCAGCTA	TACTGTCGTGGCTCTTCTTCAGCTGA	686
Db	526	TGAGTAGCGCCCAACGAGCTGTGCACTCT	CTCTCTCTGCTGCCTTCACCTTGCCAGCTGG	467
QY	687	TGATGTC	694	
Db	466	GGAAGCTC	459	

RESULT 14
US-10-204-708-81
Sequence 81, Application US/10204708
Patent No. 6677731
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENROCK, Christian
APPLICANT: BERRIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/204,708
PRIOR FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: PCT/EP01/03971
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 81
LENGTH: 5476
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-81
Query Match 2.7%; Score 36.4; DB 4; Length 5476;
Best Local Similarity 50.6%; Pred. No. 1.2;
Matches 88; Conservative 0; Mismatches 86; Indels 0; Gaps 0;
QY 1151 GGTGTACAAGTGTATGTCGCAATGACCTTTTGTAAAGATGATTAATGCAAGT 1210
DB 85 GTTATTGAATATTTGTTTATTGTTAGTTTTTTTATTTATTTATTTATGTTAAT 144
QY 1211 AGTTATCTAATCTGTCGCAATGACCTTCTATCCTTGACTTAGATTCTGCGAGAGA 1270
DB 145 TTTTGAATTTTGTAAATGAAATTTTATTTTATTTTAAATTTATTTAAAGT 204
QY 1271 AGTGAAATAGCAGCCCCCAAAATTAATTTATGAAAAA 1324
DB 205 AGTAAGTTAGATTATATGTTATTTAAAAAAGAAAAA 258

RESULT 15
US-08-311-731A-126/C
Sequence 126, Application US/08311731A
Patent No. 6583266
GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS
APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LABRAE FOR
NUMBER OF SEQUENCES: 411
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOJF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C0044/7125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
TELEFAX: 617/720-2441
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 42157 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: MYCOBACTERIUM LEPRAE
US-08-311-731A-126
Query Match 2.7%; Score 36.4; DB 4; Length 42157;
Best Local Similarity 53.5%; Pred. No. 4.3; Indels 0; Gaps 0;
Matches 76; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
QY 3 TGAGAGCTCTGCTCTTCTTCTTAAAGCGGCGCCGAGAGCCATGCGGAGTCCGAC 62
DB 4650 TGCCCGCTTATCTTGTACGCGGAGTCATCCGAGTATGTAACCGGAGATGAGACA 4591
QY 63 ACTGGGAGGAGTACCGACCAACCCGACCGCTGTGGGCTGGGAGAAAGTTGCTGA 122
DB 4590 CCTGTGCAAGCTTGTACCCATGACCGGCTGGCGAATGGGTGCTAAGAAAGCTGCTGT 4531
QY 123 TTTGAGAGAGAGCAGCAGCGCC 144
DB 4530 TGATGCCAGCAGCGGCTGCC 4509

Search completed: June 17, 2004, 14:14:56
Job time : 129 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 17, 2004, 10:34:30 / Search time 579 Seconds
(without alignment)
9714.360 Million cell updates/sec

Title: US-09-441-242A-1
Perfect score: 1324
Sequence: 1 cttgagagagcctcgcctt.....catgaaaaaaaaaaaaaa 1324

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 3373863 seqs, 212409041 residues
Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N GeneSeq_29Jan04:*
1: GeneSeqn1980s:*
2: GeneSeqn1990s:*
3: GeneSeqn2000s:*
4: GeneSeqn2001s:*
5: GeneSeqn2001bs:*
6: GeneSeqn2002s:*
7: GeneSeqn2003as:*
8: GeneSeqn2003bs:*
9: GeneSeqn2003cs:*
10: GeneSeqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1324	100.0	1324	2	AAT18876 Human TCL
2	1324	100.0	1324	4	AAK54940 Human hae
3	1324	100.0	1324	6	ABG73183 DNA encod
4	1324	100.0	1324	6	ABG73184 DNA encod
5	1280	96.7	1368	8	AA158979 Human pol
6	1280	96.7	1368	8	ADB48961 Novel hum
7	1177	88.9	1235	4	AA160765 Human pol
8	819.4	61.9	4922	2	AA118877 Human TCL
9	511	38.6	561	3	AA889670 Human T c
10	285	21.5	285	4	AAK54596 Human hae
11	285	21.5	285	4	AAK54743 Human hae
12	283.4	21.4	285	4	AAK54793 Human hae
13	283.4	21.4	285	4	AAK54693 Human hae
14	283	21.4	318	4	AAK54724 Human hae
15	283	21.4	318	4	AAK54566 Human hae
16	240	18.1	240	4	AAK54601 Human hae
17	235	17.0	240	4	AAK54594 Human hae
18	225	17.0	228	4	AAK54604 Human hae
19	189.8	14.3	221	4	AAK54585 Human hae
20	167.8	12.7	3716	7	ABZ09916 Human 5'
21	107.6	8.1	3716	7	ABZ10065 Haematopo
22	107.6	8.1	6716	6	ABLJ3782 Human imm
23	102	7.7	3716	7	ABZ10066 Haematopo

C	24	102	7.7	6716	6	ABLJ3783	AbJ3783 Human imm
C	25	88.6	6.7	3716	7	ABZ10211	AbZ10212 Haematopo
C	26	81.2	5.6	3716	7	ABZ10212	AbZ10212 Haematopo
C	27	74.8	5.6	520	6	ABQ51088	AbQ51088 Oligonuc1
C	28	74.8	5.6	520	6	ABQ51089	AbQ51089 Oligonuc1
C	29	67.8	5.1	520	6	ABQ51087	AbQ51087 Oligonuc1
C	30	67.8	5.1	520	6	ABQ51086	AbQ51086 Oligonuc1
C	31	65	4.9	560	2	AAT18875	AAT18875 Human TCL
C	32	65	4.9	560	2	ABG73185	AbG73185 Human trs
C	33	62.8	4.7	1152	3	AAH75822	AAH75822 Nucleotid
C	34	60	4.5	60	6	ABN39452	ABN39452 Human spl
C	35	51.4	3.9	2000	7	ADA71938	Ada71938 Rice gene
C	36	50.6	3.8	6486	3	AAH75823	AAH75823 Nucleotid
C	37	50	3.8	50	6	ABZ03492	AbZ03492 Human leu
C	38	48.2	3.6	2000	7	ADA71938	Ada71938 Rice gene
C	39	47.2	3.6	5840	8	ACC83409	Acc83409 LBP-32 hy
C	40	42.2	3.2	906	3	AAH78162	AAH78162 Human can
C	41	42.2	3.2	1437	4	AAH37772	AAH37772 Human col
C	42	42.2	3.2	3375	6	ABQ54651	AbQ54651 Human ova
C	43	41.8	3.2	110000	4	AAI99682_23	Continuation (24 o
C	44	41.8	3.2	110000	4	AAI99683_23	Continuation (24 o
C	45	41.4	3.1	3799	6	AAH16458	AAH16458 Corn cDNA

ALIGNMENTS

RESULT 1
AAT18876
ID AAT18876 standard; cDNA; 1324 BP.

AC AAT18876;

DT 23-AUG-1996 (first entry)

DE Human TCL-1 cDNA.

KW TCL-1; chromosome-14; leukaemia; lymphoma; gene therapy; ss.

OS Homo sapiens.

FN Key Location/Qualifiers

FT CDS 49..390

FT CDS /*tag= a

PF 23-OCT-1995; 95WO-US013663.

PR 27-OCT-1994; 94US-00330272.

PA (UYJE-) UNIV JEFFERSON THOMAS.

PA (RAGG-) RAGGIO-ITALGENE SPA.

PI Russo G, Croce CM;

PI WPI; 1996-239444/24.

DR P-PSDB; AAR94974.

XX New TCL-1 protein and gene associated with chromosome 14 abnormalities -

PT useful to develop probe, for detection, treatment and prevention of

PT diseases such as T-cell leukaemia(s) and lymphoma(s).

PS Claim 4; Page 66-67; 105pp; English.

CC A cDNA clone (AAT18876) codes for human TCL-1 protein (AAR94974). It was

CC obt'd. from the ALL1 pre-B-cell line cDNA library by screening with probes

CC derived from the human genomic library PI prep'd. from human placental

CC DNA. The cDNA was incorporated into vector pORF30 to allow expression in

CC Escherichia coli. A TCL-1 genomic sequence (AAT18877) has also been

CC identified. The TCL-1 gene is expressed at high levels in leukemic cells

PT e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and
 PT Hodgkin's and T/B cell non-Hodgkin's lymphoma.
 XX
 PS Claim 31, Page 503-504, 1252pp: English.

XX The present invention relates to compositions and methods for the
 CC detection, diagnosis and therapy of haematological malignancies. The
 CC present sequence is the coding sequence of a human haematological
 CC malignancy related antigen. The methods of the present invention comprise
 CC detecting the presence of haematological malignancy related antigen(s) in
 CC a sample obtained from the patient (an increased level of the
 CC polypeptide, compared to an unaffected individual, is indicative of an
 CC increased risk). Haematological malignancies which can be treated using
 CC the present invention are chronic lymphocytic leukaemia, lymphoma,
 CC follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B
 CC cell non-Hodgkin's lymphoma

XX Sequence 1324 BP, 293 A; 376 C; 348 G; 307 T; 0 U; 0 Other;

Query Match 100.0%; Score 1324; DB 4; Length 1324;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 1324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGAGAGGCTCTGCTCTTCTTGAAGCGGCCGAGAGACGCCATGGCCGAGTCCCG 60
 DB 1 CTTGAGAGGCTCTGCTCTTCTTGAAGCGGCCGAGAGACGCCATGGCCGAGTCCCG 60
 QY 61 ACACCTGGGAGAGGAGTCACCGACCCGAGCCGCTGTGGGCTGGGAGAAAGTTGCTG 120
 DB 61 ACACCTGGGAGAGGAGTCACCGACCCGAGCCGCTGTGGGCTGGGAGAAAGTTGCTG 120
 QY 121 TATTGAGCGAGAGCAGCAGCCGCTGCTTAAACATCGAGATTAAGATAGTTA 180
 DB 121 TATTGAGCGAGAGCAGCAGCCGCTGCTTAAACATCGAGATTAAGATAGTTA 180
 QY 121 TATTGAGCGAGAGCAGCAGCCGCTGCTTAAACATCGAGATTAAGATAGTTA 180
 DB 121 TATTGAGCGAGAGCAGCAGCCGCTGCTTAAACATCGAGATTAAGATAGTTA 180
 QY 181 CAGTTACGGGTGCTCTTCTGCGGAGACGTCGCTCGGGAGGCTTATGACCCCAACC 240
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 QY 241 CAGATAGGCCCAAGCTGCTGCTATCATGTGGAGCTCTTACCTGATGACGATACCGA 300
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 QY 301 TCCCTCAGCTCAGTTTCTGCGGCTTATGACCAATCAAGATGAGGCGGTGAGAGAC 360
 DB 301 TCCCTCAGCTCAGTTTCTGCGGCTTATGACCAATCAAGATGAGGCGGTGAGAGAC 360
 QY 361 ATGCTTCTGAGCTGCTGCTCAGATGATGATGCTTGGAGACACTGCTCTCCCTT 420
 DB 361 ATGCTTCTGAGCTGCTGCTCAGATGATGATGCTTGGAGACACTGCTCTCCCTT 420
 QY 421 CACCCAGGAGGCTGAGCTGAGCCAGCTCAATGAGGAGTGTGTCTTCTGTTCACTTC 480
 DB 421 CACCCAGGAGGCTGAGCTGAGCCAGCTCAATGAGGAGTGTGTCTTCTGTTCACTTC 480
 QY 481 GTTTACTATGCTGCTGTCTTCTTCCACCAAGCTGGGGGTGGGAGAAATGACACAGAG 540
 DB 481 GTTTACTATGCTGCTGTCTTCTTCCACCAAGCTGGGGGTGGGAGAAATGACACAGAG 540
 QY 541 GATGAGCTCTACCAAGGAGCTGACAGACCTGCTGATGACCACTCTGCTCCCTTACAC 600
 DB 541 GATGAGCTCTACCAAGGAGCTGACAGACCTGCTGATGACCACTCTGCTCCCTTACAC 600
 QY 601 TACCACTCTCTCCAAAGAGATTCATTGGCAAGCTTCTTCAAGTGGCCAGCTATAC 660
 DB 601 TACCACTCTCTCCAAAGAGATTCATTGGCAAGCTTCTTCAAGTGGCCAGCTATAC 660
 QY 661 CTGTGCTCGGCTTTTCTCAGCTGATGATGATGCTTCAAGCTTCTTCTGCTCTGTC 720
 DB 661 CTGTGCTCGGCTTTTCTCAGCTGATGATGATGCTTCAAGCTTCTTCTGCTCTGTC 720
 QY 721 CCTCAGACACTAGATTTCAATGTTGACACCACTCAGCTCCGTAAGCTTGTGAGAAC 780
 DB 721 CCTCAGACACTAGATTTCAATGTTGACACCACTCAGCTCCGTAAGCTTGTGAGAAC 780

DB 721 CCTCAGACACTAGATTTCAATGTTGACACCACTCAGCTCCGTAAGCTTGTGAGAAC 780
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 DB 781 CAGCCGATTCACCTGAGAGAGACCTCTGAAAACCTTGAGCCAGTGTCTTCAATGTTGCTA 840
 QY 841 CGCCGATCTGAAAACAGCCCTGCAAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
 DB 841 CGCCGATCTGAAAACAGCCCTGCAAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
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 DB 901 CCTGCTGCTGAAAACAGCCCTGCAAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
 QY 961 GAAAGGCTGAAAAGAGCCCTTATCTGTGCTCAGAGCTCAGAACCTCTGGGTCACTGCT 1020
 DB 961 GAAAGGCTGAAAAGAGCCCTTATCTGTGCTCAGAGCTCAGAACCTCTGGGTCACTGCT 1020
 QY 1021 CCACATCCCGGAGAGCAG 1080
 DB 1021 CCACATCCCGGAGAGCAG 1080
 QY 1081 CCTTGGCTTGCCTCAGCTGAGAAAAGGATAGAGGTTGGGTTTCCCTTTATAGATGCT 1140
 DB 1081 CCTTGGCTTGCCTCAGCTGAGAAAAGGATAGAGGTTGGGTTTCCCTTTATAGATGCT 1140
 QY 1141 CAGGACCTGCTGCTTACAAAGTTGATGCTGATGAAATCTTTTGTAAATGATGATTA 1200
 DB 1141 CAGGACCTGCTGCTTACAAAGTTGATGCTGATGAAATCTTTTGTAAATGATGATTA 1200
 QY 1201 AATGCAAGATGATTTATCTTAACTTGTGCGGAAACAGCTTATCTTATGATGATCT 1260
 DB 1201 AATGCAAGATGATTTATCTTAACTTGTGCGGAAACAGCTTATCTTATGATGATCT 1260
 QY 1261 GGTGAGAGAAAGTGAATAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
 DB 1261 GGTGAGAGAAAGTGAATAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
 QY 1321 AAAA 1324
 DB 1321 AAAA 1324

RESULT 3
 ABS73183
 ID ABS73183 standard; DNA, 1324 BP.
 XX
 AC ABS73183;
 XX
 DT 04-DEC-2002 (first entry)
 XX
 DE DNA encoding human translocation inv14(q11, q32) protein #1.
 XX
 KW Chromosome aberration; oncogenic fusion protein; cancer;
 KW proliferative disease; cellular protein isoform; heat shock protein 90;
 KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
 KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
 KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
 KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
 KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
 KW rhabdomyosarcoma; synovial sarcoma; viral infection; gene; ds.
 XX
 OS Homo sapiens.
 XX
 FN MO200269900-A2.
 PD 12-SEP-2002.
 XX
 PF 01-MAR-2002; 2002MO-US006518.
 XX
 PR 01-MAR-2001; 2001US-0272751P.
 XX
 PA (CONF-) CONFORMA THERAPEUTICS CORP.

XX Fritze LC, Burrows RJ;
 PI WPI: 2002-698710/75.
 DR P-PSDB; AB95020.
 XX
 PT Treating genetically-defined disease associated with chromosomal
 PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
 PT diseases, involves administering an inhibitor of heat shock protein 90.
 XX
 PS Disclosure; Page 103-104; 389pp; English.
 CC The invention describes a method of treating genetically-defined disease
 CC associated with chromosomal aberrations yielding oncogenic fusion
 CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
 CC cell population, treating proliferative diseases associated with mutant
 CC protein or cellular protein isoforms (II) dependent on heat shock protein
 CC (HSP)-90, or selectively treating cells expressing (II) involving
 CC administering HSP90-inhibitor. The method is useful for treating
 CC genetically-defined disease with chromosomal aberration yielding
 CC oncogenic fusion protein, treating cancerous cells containing fusion
 CC protein in heterogeneous cell population, treating proliferative disease
 CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
 CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
 CC p53), or selectively treating cells expressing mutant protein or cellular
 CC protein isoform in a patient heterozygous for (II). The method is useful
 CC for treating a disease e.g. haematopoietic disorder such as T or B cell
 CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CML,
 CC or a disease characterised by a solid tumour such as papillary thyroid
 CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
 CC synovial sarcoma. The method is also useful for treating viral
 CC infections. This represents the DNA sequence of a chromosome aberration
 XX
 S0 Sequence 1324 BP; 293 A; 376 C; 348 G; 307 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1324; DB 6; Length 1324;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 481 GTTACTATGCTGTGTCTTCTCCACACGCTGGGCTTGGAGAAATGACACAGAG 540
 Qy 541 GATAGCTTACCCAGGCTGTGAGAGACTGCTGTAGCCACTTGTGCTTACAC 600
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 Qy 601 TACACATCCCAAGAGAGATTCATTTGGCAGAGCTTTCCAGTGGCCAGCTATAC 660
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 Qy 721 CTTCAACGACTGTGATTTTATTTGACACCCACTGAGCTCGTAACTTGTGAGAAC 780
 Db 721 CTTCAACGACTGTGATTTTATTTGACACCCACTGAGCTCGTAACTTGTGAGAAC 780
 Qy 781 CAGCCGATTCACCTGAGAGAGACTGCTGAAACCTTGGACAGTGTCTGACATGTCCTA 840
 Db 781 CAGCCGATTCACCTGAGAGAGACTGCTGAAACCTTGGACAGTGTCTGACATGTCCTA 840
 Qy 841 CGCTGATGTAAACAGCTGTGAAACGCTGCTGCGGTAAACAGCCTGCAACGCTG 900
 Db 841 CGCTGATGTAAACAGCTGTGAAACGCTGCTGCGGTAAACAGCCTGCAACGCTG 900
 Qy 901 CTTGCTGCTTAAACAGCTGTGCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
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 Db 1321 AAAA 1324
 RESULT 4
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 AC ABS73184;
 XX
 DT 04-DEC-2002 (first entry)
 XX
 XX DNA encoding human translocation inv14(q11; q32) protein #2.
 DE Chromosome aberration; oncogenic fusion protein; cancer;
 KW Proliferative disease; cellular protein isoform; heat shock protein 90;
 KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
 KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;

Db	963	GCCTCCCGTAAACACAGCCTGCAAAAGCCTGCTGCCACACAGATTACGTGAGCTCAA	962
Qy	960	GGAAAGGCGCTGAAAGAAGGCCCTTATCTGTGCTCAGAGACTCADAAGCCTGGGTCACTGG	101
Db	963	GGAAAGGCGCTGAAAGAAGGCCCTTATCTGTGCTCAGAGACTCADAAGCCTGGGTCACTGG	102
Qy	1020	TCACATCTCCGGGAGCGCAGCAGAGAGGCCAGGCCGCGAGACCCCTGTGGATGAGCCCTCAGA	107
Db	1023	TCACATCTCCGGGAGCGCAGCAGAGAGGCCAGGCCGCGAGACCCCTGTGGATGAGCCCTCAGA	108
Qy	1080	ACCCTTGCGCTGGCCACGTCGGAAGAGGATAGAGTTGGGGTTTCCCCCCTTTATGATG	113
Db	1083	ACCCTTGCGCTGGCCACGTCGGAAGAGGATAGAGTTGGGGTTTCCCCCCTTTATGATG	114
Qy	1139	G-TCACGACCTGGGTG-TTACAAAGTTGTATGTGGCATGAATACCTTTTGTATGATGTTG	119
Db	1143	GTTCCAGCAGCCGCGGTGTTTACAAAGTTGTATGTGGCATGAATACCTTTTGTATGATGTTG	120
Qy	1197	ATTAAATGCAGATGATGTTATCTAA	1221
Db	1203	ATTAAATGCAGATGATGTTATCTAA	1227

ID	AA118877	standard; DNA; 4922 BP.
XX	AA118877;	
XX	23-AUG-1996	(first entry)
XX	Human TCL-1 gene.	
XX	TCL-1; chromosome-14; leukaemia; lymphoma; gene therapy; ss.	
XX	Homo sapiens.	
XX	Key	Location/Qualifiers
XX	TATA_signal	422..426
XX	exon	/*tag= a
XX	exon	462..4627
XX	intron	/*tag= b
XX	intron	/label= Exon-I
XX	intron	628..2203
XX	exon	/*tag= C
XX	exon	/label= Intron-I
XX	exon	2204..2380
XX	intron	/*tag= d
XX	intron	/label= Exon-II
XX	intron	2381..2799
XX	exon	/*tag= e
XX	exon	/label= Intron-II
XX	exon	2800..2853
XX	intron	/*tag= f
XX	intron	/label= Exon-III
XX	intron	2854..3726
XX	exon	/*tag= g
XX	exon	/label= Intron-III
XX	exon	3727..4643
XX	exon	/*tag= h
XX	exon	/label= Exon-III+3'UTR
XX	W09613514-A1.	
XX	09-MAY-1996.	
XX	23-OCT-1995;	95WO-US013663.
XX	27-OCT-1994;	94US-00330272.
XX	(UTJE-) UNIV JEFFERSON THOMAS.	
XX	(RAGG-) RAGGIO-ITALGENE SPA.	

PI Russo G, Croce CM;
XX
DR WPI: 1996-239444/24.
DR P-FSDB; AAR94975.
XX
PT New TCL-1 protein and gene associated with chromosome 14 abnormalities -
PT useful to develop prods. for detection, treatment and prevention of
PT diseases such as T-cell leukaemia(s) and lymphoma(s).
XX
XX
PS Disclosure; Page 69-72; 105pp; English.
XX
XX The human TCL-1 gene (AAR18877) was isolated from the region between 2
CC sets of breakpoints of approx. 160 kb on the TCL-1 locus of chromosome
CC 14. The TCL-1 gene is expressed at high levels in leukaemic cells
CC carrying a t(14;14)(q11;q32) translocation or an inv(14)(q11;q32)
CC inversion. The gene, probes derived from it, antisense sequences, and the
CC encoded protein (AAR94975) can be used for the diagnosis or treatment of
CC conditions associated with increased expression of TCL-1 proteins and/or
CC with chromosome 14 abnormalities, esp. T-cell leukaemia and lymphoma
XX
XX Sequence 4922 BP; 1091 A; 1278 C; 1168 G; 1202 T; 0 U; 183 Other;

Query Match	91.9%;	Score	819.4;	DB 2;	Length	4922;			
Best Local Similarity	92.7%;	Pred.	No. 1.3e-230;						
Matches	853;	Conservative	29;	Mismatches	34;	Indels	4;	Gaps	4

Qy	396	GGTCTGGCAGCACCTGTCTCTCTTTCACCCCGAGGGCCTGAGCTGGCAGCCTTACAATGG	455
Db	3726	GGTCTGGYAGCACCTGTCTCTTTCACCCGAGGGCCTGAGCTGGCAGCCTTACAATGG	3785
Qy	456	GGATGTTGTCTTCTGTTCACCTTCGTTACTATAGCCGTGTCTTCTTCACCAAGCCTGGG	515
Db	3786	GGATGTGTGTCTTCTGTTCACCTTCGTTACTATAGTGTGTGTCTTCTTCACCAAGCCTGGG	3841
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Db	3846	GTCTGGGAGGAATGAGACAGACAGAGATGAGCTTACCCAGGGCCTGAGAGACCTGTCT	3901
Qy	575	GTAGCCCACTCTGCTCGCTTTAGCA-CTACCACTCTGCAAGAGATTCCATTYTGCA	633
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Qy	634	GAGCTTCTTCAGAGTCCCAAGCTTACTCTGTGCTCGGCTTTTCTCACTGATATGCT	693
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Qy	694	CTTAGAGCTCTTCTGTGCTCCCTTCTGTGCTGCTCAAGACATGATTTCAATGTGCAACCC	753
Db	4026	CNNAGGCTCTTCTGTGCTCCCTTCTGTGCTGCTCAAGACATGATTTCAATGTGCAACCC	4081
Qy	754	ACTCAGCTCCGTGAATCTTGTAGAAACAAGCCGATTCACTGAGCAGACCTCTGAAC	813
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Qy	814	CTGACACAGTGTCTCATGTGTCTACGCTGCATGTAAACAGCCTGCAACGCTGCC	873
Db	4146	CTGACACAGTGTCTCATGTGTCTACGCTGCATGTAAACAGCCTTCAACGCTGCC	4201
Qy	874	TGCGCGTAAACAGCGCTGCAAA-CTGCGCTGCCGCTTAAACAAGCGTGTCAAAAGCTGCT	932
Db	4206	TGCGCGTAAACAGCMSRYMAAGSTGTSMWRCCGTAAACAGCGTGTCAAAAGCTGCT	4261
Qy	933	GCCACACAGGTTTCACTGACGCTCAAGAGAAAGCGCTTAAAGAGACCTTATCTGTCT	992
Db	4266	GCCACACAGGTTTCACTGACGCTCAAGAGAAAGMCTAAARRBAGCCTTATCTGTCT	4322
Qy	993	AGGACTAGAAAGCTCTGGGTCAAGTGTCTCATCTCCGGGACGACAGAGAGCCAGGCC	1051
Db	4326	AGGACTAGAAAGCTCTGGGTCAAGTGTCTCATCTCCGGGACGAGNAGAGAGCCAGGCC	4381
Qy	1053	GGCGAGCCCTGTGATAGAGCCTTCAGAACCTTGTGGCTTGCCCACTGGAATAAGGATAGA	1111
Db	4386	GGCGAGCCCTGTGATAGAGCCTTCAGAACCTTGTGGCTTGCCCACTGGAATAAGGATAGA	4441

QY 1113 GGTGGGTTTCCCCC-TTTATAGATGTCACGCACTGGGTGTTACAAAGTTGATG 1171
 CC |||||
 CC inflammation, allergies, Chediak-Higashi Syndrome (CHS), Alzheimer's
 Db 4446 GGTGGGTTTCCCCC-TTTATAGATGTCACGCACTGGGTGTTACAAAGTTGATG 4505
 CC |||||
 CC disease, Parkinson's disease, Huntington's disease, diabetes, digestion
 QY 1112 GATATAAATCTTTTGTATGATGATTAAATGCAAGATGTTATCTTAAGTCTGCGC 1231
 CC |||||
 CC disorders and wound healing disorders. The nucleic acids, antagonists or
 Db 4506 GATATAAATCTTTGATGATGATTAAATGCAAGATGTTATCTTAAGTCTGCGC 4565
 CC |||||
 CC agents of Exo proteins are useful in gene therapy. The nucleic acids
 QY 1232 AATCAGCTTCTATCCTTGATGATGATTCGTGTGAGAGAGATGAGATAGCGAGCCCA 1291
 |||||
 Db 4566 AATCAGCTTCTATCCTTGATGATTCGTGTGAGAGAGATGAGATAGCGAGCCCA 4625
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 QY 1292 AATATAAATATTCATGGA 1311
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 Db 4626 NATATAAATATTCATGGA 4645
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 AAA89670
 ID AAA89670 standard; cDNA; 561 BP.
 XX
 AC AAA89670;
 XX
 DT 08-JAN-2001 (first entry)
 XX
 DE Human T cell leukemia/lymphoma 1 nucleotide sequence.
 XX
 KW Exocytosis pathway protein; Exo protein; antiparkinsonian; antidiabetic;
 KW antiallergic; antispasmodic; neuroprotective; anticonvulsant;
 KW vulnerability; asthma; inflammation; allergy; Chediak-Higashi Syndrome; CHS;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; diabetes;
 KW digestion disorder; wound healing disorder; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200043419-A2.
 XX
 PD 27-JUL-2000.
 XX
 PF 20-JAN-2000; 2000WO-US001431.
 XX
 PR 20-JAN-1999; 99US-0116534P.
 PR 26-JAN-1999; 99US-0117274P.
 PR 26-JAN-1999; 99US-0117308P.
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 PR 26-JAN-1999; 99US-0117312P.
 PR 01-FEB-1999; 99US-0118177P.
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 PR 09-FEB-1999; 99US-0119286P.
 PR 11-FEB-1999; 99US-0119759P.
 PR 11-FEB-1999; 99US-0119988P.
 XX
 PA (RIGE-) RIGEL PHARM INC.
 XX
 PI Luo Y;
 XX
 DR WPI; 2000-482908/42.
 XX
 PT New nucleic acids encoding Exo proteins which are useful in the
 PT diagnosis, treatment or prevention of exocytosis-mediated disorders such
 PT as asthma, inflammation and allergies.
 XX
 PS Disclosure; Page 251; 305pp; English.
 XX
 CC The present sequence encodes a polypeptide which is associated with the
 CC exocytosis pathway. cDNA molecules encoding proteins involved in
 CC exocytosis have been isolated by yeast one-hybrid and two-hybrid
 CC screening. Novel proteins, termed Exo proteins, have been identified that
 CC interact with known exocytosis-associated proteins such as GS27, alpha
 CC snap, unc18-1, Vamp3, snap-23, and the rab family of proteins. Exo
 CC proteins and their agonists and antagonists are useful in the diagnosis,

CC treatment or prevention of exocytosis-mediated disorders such as asthma,
 CC inflammation, allergies, Chediak-Higashi Syndrome (CHS), Alzheimer's
 CC disease, Parkinson's disease, Huntington's disease, diabetes, digestion
 CC disorders and wound healing disorders. The nucleic acids, antagonists or
 CC agents of Exo proteins are useful in gene therapy. The nucleic acids
 CC are also useful for generating transgenic or knock-out animals which can
 CC be used in the development and screening of therapeutically useful
 CC reagents
 XX
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 Best Local Similarity 98.4%; Pred. No. 4.5e-140;
 Matches 555; Conservative 0; Mismatches 5; Indels 4; Gaps 4;
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 QY 284 CTGATGACGATACCGATCTCTGAGCTCCAGTCTTTCGGCGCTTAAGTACCATCAAGA 343
 Db 181 CTGATGACGATACCGATCTCTGAGCTCCAGTCTTTCGGCGCTTAAGTACCATCAAGA 240
 QY 344 TTACGCGCGTGGAGACATCTCTGAGCTGTGCGACATGATGATGATGATGATGATG 403
 Db 241 TTACGCGCGTGGAGACATCTCTGAGCTGTGCGACATGATGATGATGATGATGATG 300
 QY 404 CAGCACTGTCTCTTTACACCCAGGAGCTGAGCCTGAGCCAGCTCAATGGGATGTTG 463
 Db 301 CAGCACTGTCTCTTTACACCCAGGAGCTGAGCCTGAGCCAGCTCAATGGGATGTTG 360
 QY 464 TGTTCGTTCACCTTCGTTTACTATGCTGTGTCTTTCACACAGCTGGGCTGGGA 523
 Db 361 TGTTCGTTCACCTTCGTTTACTATGCTGTGTCTTTCACACAGCTGGGCTGGGA 420
 QY 524 GGAATGACAGACAGAGATGAGCTTACCCAGGAGCTGACAGACCTGTGAGCCAC 583
 Db 421 GGAATGACAGACAGAGATGAGCTTACCCAGGAGCTGACAGACCTGTGAG-CCAC 479
 QY 584 TCTGCTGCGCTTACGATCACTCTCTGCAAGAGAGATTCATTTGGACAGCTTCTT 643
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 Db 538 CAGGTG-CCANCTATNCTGTGCC 560
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 ID AAK54596 standard; cDNA; 285 BP.
 XX
 AC AAK54596;
 XX
 DT 13-NOV-2001 (first entry)
 XX
 DE Human haematological malignancy-related antigen coding sequence #321.
 XX
 KW Human; cytostatic; vascular; gene therapy; vaccine; lymphoma;
 KW haematological malignancy; antigen; chronic lymphocytic leukemia;
 KW follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200164886-A2.

[illegible]

AC	AAKS4743;
DT	13-NOV-2001 (first entry)
DE	Human haematological malignancy-related antigen coding sequence #468.
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KW	Human; cytosolic; vascular; gene therapy; vaccine; lymphoma; haematological malignancy; antigen; chronic lymphocytic leukemia; follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma; ss.
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OS	Homo sapiens.
PV	WO200164886-A2.
XX	
PD	07-SEP-2001.
PF	01-MAR-2001; 2001WO-US007272.
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PR	01-MAR-2000; 2000US-0186126P. 17-MAR-2000; 2000US-0190479P. 27-APR-2000; 2000US-0200545P. 28-APR-2000; 2000US-0200303P. 28-APR-2000; 2000US-0200779P. 01-MAY-2000; 2000US-0200999P. 04-MAY-2000; 2000US-0202084P. 22-MAY-2000; 2000US-0206201P. 14-JUL-2000; 2000US-0218950P. 03-AUG-2000; 2000US-0222903P. 04-AUG-2000; 2000US-0223416P. 07-AUG-2000; 2000US-0223378P.
PA	(CORI-) CORIXA CORP.
PI	Gaiger A, Algate PA, Mannion J;
XX	
DR	WPI; 2001-514842/56.
XX	
PT	Compositions and methods for the detection of hematological malignancies, e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and Hodgkin's and T/B cell non-Hodgkin's lymphoma.
XX	
PS	Claim 31; Page 454; 1252pp; English.
XX	
CC	The present invention relates to compositions and methods for the detection, diagnosis and therapy of haematological malignancies. The present sequence is the coding sequence of a human haematological malignancy related antigen. The methods of the present invention comprise detecting the presence of haematological malignancy related antigen(s) in a sample obtained from the patient (an increased level of the polypeptide, compared to an unaffected individual, is indicative of an increased risk). Haematological malignancies which can be treated using the present invention are chronic lymphocytic leukaemia, lymphoma, follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B cell non-Hodgkin's lymphoma
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Best Local Similarity	100.0%; Pred. No. 1.7e-73;
Matches 285; Conservative	0; Mismatches 0; Indels 0; Gaps 0
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Dz	285 CTGATGATGGTCTTCAGCCTCTTTGTGCCCTTGTCCTCAAGACAAGTAATTTC 226
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Dz	225 TGTTGCACACCCTCACTCAGCTCGTGAATTGTAGAACAAGCCGATTCACCTGACAG 166
Dy	802 ACCCTGAAACCCCTGAGACCATGTGTCACATGAGCGTCAAGCCGATTAACAGGCT 861
Dz	165 ACCCTGAAACCCCTGAGACCATGTGTCACATGAGCGTCAAGCCGATTAACAGGCT 106

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Searched: 3470272 seqs, 2167151695 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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41: em_hcgo_other: *

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and is derived by analysis of the total score distribution.

SUMMARIES

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2	1324	100.0	1324	6 AX237689	AX237689 Sequence
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4	1280	96.7	1368	6 AR339380	AR339380 Sequence
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6	1187	89.7	1231	9 BC005831	BC005831 Homo sapi
7	925	69.9	925	11 G26659	G26659 human STS S
8	902.4	68.2	166308	2 CNS01DX2	AL139020 Human chr
9	894	67.5	938	9 BC009502	BC009502 Homo sapi
10	894	67.5	938	9 BC009891	BC009891 Homo sapi
11	819.8	61.9	4922	6 AR086521	AR086521 Sequence
12	285	21.5	285	6 AX237345	AX237345 Sequence
13	285	21.5	285	6 AX237492	AX237492 Sequence
14	283.4	21.4	285	6 AX237442	AX237442 Sequence
15	283.4	21.4	285	6 AX237542	AX237542 Sequence
16	283	21.4	318	6 AX237315	AX237315 Sequence
17	283	21.4	318	6 AX237473	AX237473 Sequence
18	240	18.1	240	6 AX237350	AX237350 Sequence
19	235	17.7	240	6 AX237343	AX237343 Sequence
20	225	17.0	228	6 AX237353	AX237353 Sequence
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ALIGNMENTS

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DEFINITION Sequence 1 from patent US 5985598.
ACCESSION AR086519
VERSION AR086519.1 GI:10013285
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1324)
AUTHORS Russo,G. and Croce,C.M.
TITLE TCP-1 gene and protein and related methods and compositions
JOURNAL Patent: US 5985598-A 1 16-NOV-1999;
FEATURES Location/Qualifiers

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RESULT 2
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LOCUS AX237689
DEFINITION Sequence 665 from Patent WO0164886.
ACCESSION AX237689
VERSION AX237689.1 GI:15797243
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 Gaiger, A., Algate, P. A. and Mannion, J.
Compositions and methods for the detection, diagnosis and therapy
of hematological malignancies
Patent: WO 0164886-A 665 07-SEP-2001;
JOURNAL CORIXA CORPORATION (US)
FEATURES
Location/Qualifiers
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/mol_type="unassigned DNA"
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ORIGIN

Query Match 100.0%; Score 1324; DB 6; Length 1324;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 181 CAGTTAGGAGGCTCTGCTGCTGCGGAGAGAGCTGCTTGGGAGGCTTATGACCCCA 240

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Db	481	GTTTACTATAGCTGTGTCCTTCTCCACACAGCTGGGGCTCTGGGAGAAATGACAGACAGAG	540
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Db	541	GATGAGCTTACCCAGAGGCGCTGAGGACCTGCTGTAGCCCACTCTGCTGCGCTTTAGCAC	600
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OY	1201	AATGCAAGTATGTTTATCTTAATCTTGTGTGGCAATCAGCTTCTATCCTTGACTTAAATTTCT	1260
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Db      1321  AAAA 1324  |||
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DEFINITION H.sapiens mRNA for Tcell Leukemia/lymphoma 1.
ACCESSION X82240
VERSION   X82240.1 GI:624960
KEYWORDS  TCL1 gene.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
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           Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS  Virgilio, L., Narducci, M.G., Isobe, M., Billips, L.G., Cooper, M.D.,
          Croce, C.M. and Russo, G.
JOURNAL  Identification of the TCL1 gene involved in T-cell malignancies
MEDLINE  Proc. Natl. Acad. Sci. U.S.A. 91 (26), 12530-12534 (1994)
PUBMED   95107991
         7809072
REFERENCE 2 (bases 1 to 1324)
AUTHORS   Russo, G.
TITLE     Direct Submission
JOURNAL   Submitted (19-OCT-1994) G. Russo, Raggio-Italgene SpA, Via delle
Antille 29, 00040 Pomezia, Rome, ITALY
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QY      121 TATTGGACGAGAACGACGCGCTGGCTGCCCTTAACATCGAGATAAAGATAGTTA 180
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Db 1201 AATGCAAGATGATTTATCTAACTTGTGCGCAATCAGCTTCTTCTTGAAGTCT 1260
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Db 1321 AAAA 1324
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DEFINITION Sequence 871 from patent US 6569662.
ACCESSION AR339380
VERSION AR339380.1 GI:33726237
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1368)
AUTHORS Tang, Y.T., Zhou, P. and Dymnac, R.T.
TITLE Nucleic acids and polypeptides
JOURNAL Patent: US 6569662-A 871 27-MAY-2003;
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Best Local Similarity 99.8%; Pred. No. 0;
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OY		847	CATGTA AACAGCCCTGC A AA CGCTG CCGGTAA ACAGCGCTGC A A AGCTGCTGCC	906
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DEFINITION		Homo sapiens T-cell leukemia/lymphoma 1a, mRNA (cDNA clone MGC:226605)		
VERSION		BC003574		
KEYWORDS		MGC.		
SOURCE		Homo sapiens (human)		
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE		1 (bases 1 to 1231)		
AUTHORS		Strausberg,R.L., Fellingsold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shemmen,C.M., Schuller,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Stachenko,L., Marinisa,K., Farmer,A.A., Rubin,G.M., Hong,L., Stacieleon,M., Soares,M.B., Bonaldo,M.F., Casavant,I.L., Scheetz,T.E., Brownstein,M.J., Udell,T.B., Toshitsuki,S., Carminci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullaly,S.J., Bosak,S.A., McSwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Wotley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Huliyil,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Patney,J., Helton,E., Kettelman,W., Madan,A., Rodriguez,S., Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y.,		

TITLE	Butterfield, G.G., Blakeasley, R.W., Touchman, J. W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmitz, R.M., Butterfield, I.S., Krzywinski, M.I., Skalski, U., Smailus, D.E., Scherer, A., Schell, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16699-16903 (2002)
JOURNAL	
MEDLINE	22388257
PubMed	12477932
REFERENCE	2 (bases 1 to 1231)
AUTHORS	Strausberg, R. Direct Submission
TITLE	Submitted (20-FEB-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
JOURNAL	
MEDLINE	NIH-MGC Project URL: http://mgc.nci.nih.gov
PubMed	Contact: MGC help desk
REFERENCE	Email: cgabs-remail.nih.gov Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLU) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@cgsc.bc.ca
AUTHORS	Steven Jones, Jennifer Aeano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letlicia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice Mcleavy, Steven Neas, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saeedi, Jacqueline Schell, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Scotc, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
JOURNAL	
MEDLINE	
PubMed	
REFERENCE	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate; 8 Row; d Column: 6 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4504510. Location/Qualifiers
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AUTHORS	1. 1231
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MEDLINE	58. 171
PubMed	/note="TCL1, MTCP1, Region: TCL1/MTCP1 family. Two related oncogenes, TCL-1 and MTCP-1, are overexpressed in T cell prolymphocytic leukemias as a result of chromosomal rearrangements that involve the translocation of one T cell receptor gene to either chromosome 14q32 or Xq28"
REFERENCE	/db_xref="CDD:pfam01840"
AUTHORS	232. 384
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http://www.systembiology.org
contact: amadan@systembiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIN ac: <http://image.llnl.gov>
Series: IRAL Plate: 3 Row: a Column: 9
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 11415027.

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ORIGIN

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Best Local Similarity 99.5%; Pred. No. 0;
Matches 1213; Conservative 0; Mismatches 0; Indels 6; Gaps 2;

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RESULT 7
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DEFINITION human STS X82240, sequence tagged site.
ACCESSION G26659
VERSION G26659.1 GI:134891
KEYWORDS STS; STS sequence; primer; sequence tagged site.

COMMENT

- Web : www.genoscope.cns.fr
On Apr 3, 2001 this sequence version replaced gi:12274871.
----- Genome Center
Center: Genoscope / Centre National de Sequencage
Center code: GS
Web site: <http://www.genoscope.cns.fr/>
Contact: SequRef@genoscope.cns.fr

The following BAC sequence is oriented from the T7 to the SP6 end.
Upstream BAC (overlapping the T7 end) : R-1070N10
Downstream BAC (overlapping the SP6 end) : R-185P18 (AC=AL13167)
----- Summary Statistics
Assembly program: Phrap; version 2.0
Quality coverage: 6.03x in Q20 bases; sum-of-contigs

Overall quality chart :

Range : bases
0 :
1 - 9 : 4
10 - 19 : 53
20 - 29 : 203
30 - 39 : 622
40 - 49 : 3717
50 - 59 : 8215
60 - 69 : 11927
70 - 79 : 27324
80 - 89 : 52859
90 - 99 : 61384

Percentage of bases with a quality value >= 40 : 99 %.

FEATURES

source

Location/Qualifiers

1.166308

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dbSTS:STS38175
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5797.10019
/note="matching EMBL:T96687
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dbSTS:STS38605
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/note="matching EMBL:R70888
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dbSTS:STS54563
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16118.16281
/note="matching EMBL:RA856757
RHdb:RH98896
dbSTS:STS68645
Identified using the e-PCR software (G. Schuler)"
46740.46885
/note="matching EMBL:H01982
RHdb:RH44550
dbSTS:STS37619
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47277.47485
/note="matching EMBL:X82240
RHdb:RH53532
dbSTS:STS26938
Identified using the e-PCR software (G. Schuler)"

STS

STS

STS

STS

STS

STS

ORIGIN

Query Match 68.2%; Score 902.4; DB 9; Length 166308;
Best Local Similarity 99.8%; Pred. No. 4.4e-240;

Matches 914; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Oy	396	GGTCTGGCAGACCTGCTCTTCAACCCAGGGGCGTGAAGCTGGACGCTCAATG	455
Db	47487	GGCTTGGCAGACCTGCTCTTCAACCCAGGGGCGTGAAGCTGGACGCTCAATG	47428
Oy	456	GGATGTTGTCTTCTGTTCACTTCTGTTAATATGCTGTTCTTCAACGCTGG	515
Db	47427	GGATGTTGTCTTCTGTTCACTTCTGTTAATATGCTGTTCTTCAACGCTGG	47368
Oy	516	GTCGGAGAGATGAGACAGAGATGAGCTTACCCAGGCGCTGAGAGACTGCTG	575
Db	47367	GTCGGAGAGATGAGACAGAGATGAGCTTACCCAGGCGCTGAGAGACTGCTG	47308
Oy	576	TAGCCCACTGCTGCTGCTTGAAGCTTCACTCTGCTGCAAGAGATTCATTGG	635
Db	47307	TAGCCCACTGCTGCTGCTTGAAGCTTCACTCTGCTGCAAGAGATTCATTGG	47248
Oy	636	GCTTCTTCAGAGTCCAGCTATACCTGCTGCTGCTGCTTCTGAGCTGATGCT	695
Db	47247	GCTTCTTCAGAGTCCAGCTATACCTGCTGCTGCTGCTTCTGAGCTGATGCT	47188
Oy	696	TCAGCTCTTCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	755
Db	47187	TCAGCTCTTCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	47128
Oy	756	TCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	815
Db	47127	TCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	47068
Oy	816	GGACGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	875
Db	47067	GGACGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	47008
Oy	876	CCGGTAAACAGCGCTGCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	935
Db	47007	CCGGTAAACAGCGCTGCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	46948
Oy	936	CACACAGTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	995
Db	46947	CACACAGTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	46888
Oy	996	ACTCAGAAAGCTCTGGGTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1055
Db	46887	ACTCAGAAAGCTCTGGGTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT	46828
Oy	1056	GAGCCCTGTGATGAGCCCTGCAACCTTGGCTTGGCCACGTGGAAGGATAGAGT	1115
Db	46827	GAGCCCTGTGATGAGCCCTGCAACCTTGGCTTGGCCACGTGGAAGGATAGAGT	46768
Oy	1116	TGGGTTTCCCCC-TTATATAGTGTGACGCACTGGGTGTTACAAAGTTGATGCA	1174
Db	46767	TGGGTTTCCCCC-TTATATAGTGTGACGCACTGGGTGTTACAAAGTTGATGCA	46708
Oy	1175	TGAATACCTTTTGAATGATGATTAATGAAGATGTTATCTAATTTGGGCAAT	1234
Db	46707	TGAATACCTTTTGAATGATGATTAATGAAGATGTTATCTAATTTGGGCAAT	46648
Oy	1235	CAGCTTATCTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT	1294
Db	46647	CAGCTTATCTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT	46588
Oy	1295	AAAAAATTTTATGGA 1310	
Db	46587	AAAAAATTTTATGGA 46572	

RESULT 9
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LOCUS BC009502 938 bp mRNA linear PRI 16-SEP-2003
DEFINITION Homo sapiens T-cell leukemia/lymphoma 1A, mRNA (CDNA clone
IMAGE:4054525), partial cds.
ACCESSION BC009502

REFERENCE 1 (bases 1 to 938)
AUTHORS Klausner,B.R., Collins,F.S., Wagner,L.H., Derge,J.G.,
Strasberg,R.D., Jordan,H., Moore,T., Wax,S.I., Wang,J., Hsieh,F.,
Alechni,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Wax,S.I., Wang,J., Hsieh,F.,
Datchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheer,T.E., Brownstein,M.J., Uedlin,T.B., Tothylski,S.,
Carninci,P., Prange,C., Rana,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullaney,S.J., Bosak,S.A., McEwan,P.J.,
McEwan,R.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hallyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettleman,M., Madan,A., Rodchenko,Y.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Rodchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,S., Myers,R.M.,
Butcherfield,Y.S., Krzywinski,M.I., Skalek,U., Smalits,D.E.,
Scherer,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL MEDLINE 2238257
PUBMED 12477932
REFERENCE 2 (bases 1 to 938)
AUTHORS Straube,R.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
On Aug 19, 2003 this sequence version replaced gi:14602756.
REMARK COMMENT
Contact: MGC help desk
Email: gcdb@nci.nih.gov
Tissue Procurement: Louis Staudt
cDNA Library Preparation: Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
<http://www.systemsbio.org>
contact: amadan@systemsbio.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettleman, Anuradha
Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 25 Row: 0 Column: 18.
Location/Qualifiers
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/note="Vector: pOTB7"

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Best Local Similarity 99.4%; Pred. No. 4.6e-238;
Matches 920; Conservative 0; Mismatches 0; Indels 6; Gaps 2;
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DB 1 CCGATCTCAAGCTTCTGCGGCTTGTAGTACACATCAAGATTGACGGGCTGGA 60
QY 357 GGACATGCTTCTGCGGCTTGTAGTACACATCAAGATTGACGGGCTGGA 416
DB 61 GGACATGCTTCTGCGGCTTGTAGTACACATCAAGATTGACGGGCTGGA 115
QY 417 CTTTACCCCAAGGCTGAGCTGCGCAGCTCAATGGGATGTTGTCTTCTTAC 476

DB 116 CTTTACCCCAAGGCTGAGCTGCGCAGCTCAATGGGATGTTGTCTTCTTAC 175
QY 477 CTTGTTTACATGCTGCTGCTTCTCCACACGCTGGGGCTGGAGGAATGACAGAC 536
DB 176 CTTGTTTACATGCTGCTGCTTCTCCACACGCTGGGGCTGGAGGAATGACAGAC 235
QY 537 AGAGATGAGCTTACACAGGAGGCTGAGGACCTGCTGAGGACCTGCTGCTTGA 596
DB 236 AGAGATGAGCTTACACAGGAGGCTGAGGACCTGCTGAGGACCTGCTGCTTGA 295
QY 597 GCATCAACCTCTGCGCAGGAGGATTCATTGGAGAGCTTCTTCAGGCTCCAGCT 656
DB 296 GCATCAACCTCTGCGCAGGAGGATTCATTGGAGAGCTTCTTCAGGCTCCAGCT 355
QY 657 ATACTGTGCTGCTGCTTCTTCTGAGTGAATGATGATGATGATGATGATGATG 716
DB 356 ATACTGTGCTGCTGCTTCTTCTGAGTGAATGATGATGATGATGATGATGATG 415
QY 717 TGTCCCTCAGACACTGATATTTATGTTGACACCCACTGAGCTCCGTGAATTTGAG 776
DB 416 TGTCCCTCAGACACTGATATTTATGTTGACACCCACTGAGCTCCGTGAATTTGAG 475
QY 777 AACACAGCCGATTCACCTGACAGAGACCTCTGAAACCTGAGCAGTGTCAATGT 836
DB 476 AACACAGCCGATTCACCTGACAGAGACCTCTGAAACCTGAGCAGTGTCAATGT 535
QY 837 GCTACGCTGATGATTAACAGGCTGCAAGGCTGCTGCTGCTGCTGCTGCTGCTG 896
DB 536 GCTACGCTGATGATTAACAGGCTGCAAGGCTGCTGCTGCTGCTGCTGCTGCTG 595
QY 897 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 956
DB 596 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 655
QY 957 CAAGAAAGGCTGAAAGAGACCTTATCTGTGCTCAGACTCAGAACTCTGGGTGAG 1016
DB 656 CAAGAAAGGCTGAAAGAGACCTTATCTGTGCTCAGACTCAGAACTCTGGGTGAG 715
QY 1017 TGTGTCACATCCCGGAGCGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1076
DB 716 TGTGTCACATCCCGGAGCGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 775
QY 1077 AGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1135
DB 776 AGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 835
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DB 836 ATGTGTCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 895
QY 1196 GATTAAATGCAAGTATGTTATCTTAA 1221
DB 896 GATTAAATGCAAGTATGTTATCTTAA 921

RESULT 11
AK086521
LOCUS AR086521 4922 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 5 from patent US 5985598.
ACCESSION AR086521
VERSION AR086521.1 GI:10013287
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4922)
AUTHORS Russo,G. and Croce,C.M.
TITLE TCl-1 gene and protein and related methods and compositions
JOURNAL Patent: US 5985598-A 5 16-NOV-1999,
FEATUES Location/Qualifiers
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Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 285 CTGGAATGATGCTTCAAGCTCTTTCTGTCCCTTCTGTCCCTCACAAGCACTAGTATTCA 226
QY 742 TGTTCACACCCACTCAGCTCCGTGAACCTTGAGNACACAGCCGATTACCTGAGCAG 801
DB 225 TGTTCACACCCACTCAGCTCCGTGAACCTTGAGNACACAGCCGATTACCTGAGCAG 166
QY 802 ACCTTGAACCCCTGAGACAGTGTCTCATATGTGTCTACGCTGATGTAACACGCT 861
DB 165 ACCTTGAACCCCTGAGACAGTGTCTCATATGTGTCTACGCTGATGTAACACGCT 106
QY 862 GCAAAAGCTGCTGCGGTAAACAGCCCTGCAAGCGCTCCCTGTAACACGCTGCG 921
DB 105 GCAAAAGCTGCTGCGGTAAACAGCCCTGCAAGCGCTCCCTGTAACACGCTGCG 46
QY 922 AAACGCTGCTGCCACACAGGTTCAAGTCAAGCTCAAGAAAG 966
DB 45 AAACGCTGCTGCCACACAGGTTCAAGTCAAGCTCAAGAAAG 1

RESULT 14
AX237442/c
LOCUS AX237442 285 bp DNA linear PAT 26-SEP-2001
DEFINITION Sequence 418 from Patent WO0164886.
ACCESSION AX237442
VERSION AX237442.1 GI:15796996
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS 1
TITLE Gaiger, A., Algate, P. A. and Mannion, J.
JOURNAL Compositions and methods for the detection, diagnosis and therapy
of hemtological malignancies
Patent: WO 0164886-A 418 07-SEP-2001;
CORIXA CORPORATION (US)
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Query Match 21.4%; Score 283.4; DB 6; Length 285;
Best Local Similarity 99.6%; Pred. No. 1,1e-67;
Matches 284; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 662 CTGGAATGATGCTTCAAGCTCTTTCTGTCCCTTCTGTCCCTCACAAGCACTAGTATTCA 741
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QY 742 TGTTCACACCCACTCAGCTCCGTGAACCTTGAGNACACAGCCGATTACCTGAGCAG 801
DB 225 TGTTCACACCCACTCAGCTCCGTGAACCTTGAGNACACAGCCGATTACCTGAGCAG 166
QY 802 ACCTTGAACCCCTGAGACAGTGTCTCATATGTGTCTACGCTGATGTAACACGCT 861
DB 165 ACCTTGAACCCCTGAGACAGTGTCTCATATGTGTCTACGCTGATGTAACACGCT 106
QY 862 GCAAAAGCTGCTGCGGTAAACAGCCCTGCAAGCGCTCCCTGTAACACGCTGCG 921
DB 105 GCAAAAGCTGCTGCGGTAAACAGCCCTGCAAGCGCTCCCTGTAACACGCTGCG 46
QY 922 AAACGCTGCTGCCACACAGGTTCAAGTCAAGCTCAAGAAAG 966
DB 45 AAACGCTGCTGCCACACAGGTTCAAGTCAAGCTCAAGAAAG 1

RESULT 15

AX237542/c
LOCUS AX237542 285 bp DNA linear PAT 26-SEP-2001
DEFINITION Sequence 518 from Patent WO0164886.
ACCESSION AX237542
VERSION AX237542.1 GI:15797096
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS 1
TITLE Gaiger, A., Algate, P. A. and Mannion, J.
JOURNAL Compositions and methods for the detection, diagnosis and therapy
of hemtological malignancies
Patent: WO 0164886-A 518 07-SEP-2001;
CORIXA CORPORATION (US)
FEATURES
source
Location/Qualifiers
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ORIGIN

Query Match 21.4%; Score 283.4; DB 6; Length 285;
Best Local Similarity 99.6%; Pred. No. 1,1e-67;
Matches 284; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 662 CTGGAATGATGCTTCAAGCTCTTTCTGTCCCTTCTGTCCCTCACAAGCACTAGTATTCA 741
DB 285 CTGGAATGATGCTTCAAGCTCTTTCTGTCCCTTCTGTCCCTCACAAGCACTAGTATTCA 226
QY 742 TGTTCACACCCACTCAGCTCCGTGAACCTTGAGNACACAGCCGATTACCTGAGCAG 801
DB 225 TGTTCACACCCACTCAGCTCCGTGAACCTTGAGNACACAGCCGATTACCTGAGCAG 166
QY 802 ACCTTGAACCCCTGAGACAGTGTCTCATATGTGTCTACGCTGATGTAACACAGCT 861
DB 165 ACCTTGAACCCCTGAGACAGTGTCTCATATGTGTCTACGCTGATGTAACACAGCT 106
QY 862 GCAAAAGCTGCTGCGGTAAACAGCCCTGCAAGCGCTCCCTGTAACACGCTGCG 921
DB 105 GCAAAAGCTGCTGCGGTAAACAGCCCTGCAAGCGCTCCCTGTAACACGCTGCG 46
QY 922 AAACGCTGCTGCCACACAGGTTCAAGTCAAGCTCAAGAAAG 966
DB 45 AAACGCTGCTGCCACACAGGTTCAAGTCAAGCTCAAGAAAG 1

Search completed: June 17, 2004, 13:09:49
Job time : 5332 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 17, 2004, 14:12:51 ; Search time 65 seconds

(without alignments)
546.516 Million cell updates/sec

Title: US-09-441-242A-2

Perfect score: 612
Sequence: 1 AECPTLGEAVTDHPDRLMAW.....VYHIKIDGVEDMLLELPDD 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 45 summaries

Database :

SPTREMBL 25: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriap: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	159	26.0	33	4 Q969P8	Q969P8 homo sapien
2	148	24.2	128	4 Q9UBQ4	Q9UBQ4 homo sapien
3	86	14.1	16	Q8XEX4	Q8XEX4 salmonella
4	84.5	13.8	107	11 Q9QXN9	Q9QXN9 mus musculus
5	83	13.6	619	16 Q8XBM3	Q8XBM3 escherichia
6	83	13.6	620	16 Q8FDM3	Q8FDM3 escherichia
7	75.5	12.3	4099	10 Q9C726	Q9C726 arabidopsis
8	74	12.3	275	16 Q9PJ22	Q9PJ22 chlamydia m
9	74	12.3	363	16 P73727	P73727 synchocyst
10	73.5	12.0	196	17 Q9YB77	Q9YB77 aeropyrum p
11	73.5	12.0	931	2 Q7WY21	Q7WY21 pseudomonas
12	71.5	11.7	727	17 Q58935	Q58935 pyrococcus
13	71.5	11.7	1156	17 Q8TK58	Q8TK58 methanosaarc
14	71	11.6	380	2 Q8VVI0	Q8VVI0 erwinia pyr
15	69	11.3	363	2 Q8VRP6	Q8VRP6 desulfocell
16	69	11.3	495	3 Q96VP7	Q96VP7 plachia angu

17	69	11.3	524	11 Q80UE9	Q80UE9 mus musculus
18	69	11.3	525	11 Q80VZ4	Q80VZ4 mus musculus
19	69	11.3	574	16 Q7UV67	Q7UV67 rhodospirillum rubrum
20	69	11.3	592	16 Q8R5U6	Q8R5U6 thermotoga
21	69	11.3	603	10 Q94E86	Q94E86 oryza sativa
22	68.5	11.2	236	9 Q9G0A6	Q9G0A6 vibrio phag
23	68.5	11.2	319	3 Q9HEC8	Q9HEC8 neurospora
24	68.5	11.2	689	16 Q8FIC7	Q8FIC7 corynebacte
25	68	11.1	213	16 Q8NRD2	Q8NRD2 corynebacte
26	68	11.1	308	5 Q9V8M5	Q9V8M5 dirosophila
27	68	11.1	550	5 Q8WQ59	Q8WQ59 trichinella
28	68	11.1	1111	16 Q8IDB8	Q8IDB8 bacillus ce
29	67.5	11.0	245	16 Q7UEB8	Q7UEB8 rhodospirillum rubrum
30	67.5	11.0	792	10 Q84PB3	Q84PB3 oryza sativa
31	67.5	11.0	1261	16 Q7URK6	Q7URK6 rhodospirillum rubrum
32	67	10.9	236	9 Q9G0A3	Q9G0A3 vibrio phag
33	67	10.9	236	9 Q9G0A7	Q9G0A7 vibrio phag
34	67	10.9	236	9 Q9FZQ3	Q9FZQ3 vibrio phag
35	67	10.9	282	6 Q86BD8	Q86BD8 callichrax
36	67	10.9	285	6 Q86BD7	Q86BD7 callichrax
37	67	10.9	323	2 Q918F5	Q918F5 vibrio mimi
38	67	10.9	345	6 Q9N269	Q9N269 callichrax
39	67	10.9	365	6 Q86BD9	Q86BD9 callichrax
40	67	10.9	365	6 Q86BD6	Q86BD6 leontopithec
41	67	10.9	508	4 Q9NMR4	Q9NMR4 homo sapien
42	67	10.9	629	4 Q9NMG4	Q9NMG4 homo sapien
43	67	10.9	778	4 Q9BVF1	Q9BVF1 homo sapien
44	67	10.9	882	11 Q8BKJ9	Q8BKJ9 mus musculus
45	67	10.9	1054	16 Q89VP8	Q89VP8 bradyrhizob

ALIGNMENTS

RESULT 1	Q969P8	PRELIMINARY:	PRT:	33 AA.
ID	Q969P8			
AC	Q969P8			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	Similar to T-cell leukemia/lymphoma 1A (Fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=B-cell;			
RA	Strausberg R.;			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC009502; AA009502.1; -			
DR	EMBL; BC009891; AA009891.1; -			
DR	InterPro; IPR004832; TCl1_MTCP1.			
DR	Pfam; PF01840; TCl1_MTCP1.1.			
DR	ProDom; PD015575; TCl1B; 1.			
FT	NON_TER			
FT	SEQUENCE 33 AA; 3834 MW; 9C79E571A6C7EEFA CRC64;			
Query Match	26.0%; Score 159; DB 4; Length 33;			
Best Local Similarity	96.9%; Pred. No. 1.1e-10;			
Matches	31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
Qy	82 RYRSSDSFVRLVYHIKIDGVEDMLLELPDD 113			
Db	2 RGRSSDSFVRLVYHIKIDGVEDMLLELPDD 33			
RESULT 2	Q9UBQ4	PRELIMINARY:	PRT:	128 AA.
ID	Q9UBQ4			
AC	Q9UBQ4			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			

DT 01-MAY-2000 (TREMblrel. 13, last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, last annotation update)
DE TCU1 / MTCPI-like 1.
GN TML1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99274532; PubMed=10344735;
RA Sugimoto J., Hatakeyama T., Narducci M.G., Russo G., Isobe M.;
RT "Identification of the TCU1/ MTCPI-like 1 (TML) gene from the region
RL next to the TCU1 locus.";
RN Cancer Res. 59:2313-2317(1999).
[2]
RP SEQUENCE FROM N.A.
RX TISUS-lymph;
MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Dichtenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uscid T.B., Toshiyuki S., Carinci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hallyk S.W.,
RA Villalón D.K., Mazny D.M., Sodergren E.O., Lu X., Gibbs R.A.,
RA Pailey U., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Mair M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]
RP SEQUENCE FROM N.A.
RX Strausberg R.;
RL Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB025274; BAA82476.1; -.
DR EMBL; AB025272; BAA82476.1; JOINED.
DR EMBL; AB025273; BAA82476.1; JOINED.
DR EMBL; AB018563; BAA76712.1; -.
DR EMBL; BC051000; AAH51000.1; -.
DR HSP; P56278; IAI1.
DR InterPro; IPR004832; TCU1_MTCPI.
DR Pfam; PF01840; TCU1_MTCPI.1.
DR ProDom; PD015575; TCU1B; 1.
SQ SEQUENCE 128 AA; 1485 MW; 6BA2CF22F62CFB4D CRC64;

Query Match 24.2%; Score 148; DB 4; Length 128;
Best Local Similarity 29.2%; Pred. No. 9.3e-09;
Matches 33; Conservative 21; Mismatches 45; Indels 14; Gaps 1;

QY 14 PDRLMAWEKRYVLDKQKAWLP-LTETIKDRLQ-----LRVLRREDVVLGR 59
DB 13 PGRMTIORPGIYEDEERTVTVVVRPNPSRRREWARASQGRYEPSTVHLQWAVHTRE 72
QY 60 PMPTQTQIGPSLLPIMQLYPDGRYRSSDSSFWRLVYAIKIDGVDMLLELPD 112
DB 73 LLSGQMPFSGQLPRAVWQLYPRKTKRADSSFWELADHGQIDSLMEQLVLTQPE 125

RESULT 3
Q8XEX4 PRELIMINARY; PRT; 618 AA.
AC Q8XEX4;
DT 01-MAR-2002 (TREMblrel. 20, Created)

DT 01-MAR-2002 (TREMblrel. 20, last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, last annotation update)
DE Glutathionylispermidine synthetase/amidase (Bifunctional;
DE glutathionylispermidine synthetase, glutathionylispermidine
DE amidase).
GN GSP OR T3060 OR STM3139 OR STY3130.
OS Salmonella typhi, and
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
NCBI_TaxID=601, 602;
[1]
RP SEQUENCE FROM N.A.
RX SPECIES-S.typhi; STRAIN=Ty2 / ATCC 700931;
MEDLINE=2251367; PubMed=12644504;
RA Deng W., Lion S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyanni V., Schwartz D.C., Blatter F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RL and CT18.";
RN J. Bacteriol. 185:2330-2337(2003).
[2]
RP SEQUENCE FROM N.A.
RX SPECIES-S.typhimurium; STRAIN=L72 / SSGC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulyanay E.,
RA Ryan E., Sun H., Floria L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RL L72.";
RN Nature 413:852-856(2001).
[3]
RP SEQUENCE FROM N.A.
RX SPECIES-S.typhi; STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebatina M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Felwell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jagels K.,
RA Krogan A., Larsen T.S., Leather S., Moule S., O'Garra P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrett B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RL enterica serovar Typhi CT18.";
RN Nature 413:848-852(2001).
DR EMBL; AE016844; AA070606.1; -.
DR EMBL; AE008844; AAL22013.1; -.
DR EMBL; AL627277; CAD02971.1; -.
DR InterPro; IPR007921; CHAP.
DR InterPro; IPR005484; GSP_synth.
DR Pfam; PF05257; CHAP; 1.
DR Pfam; PF03738; GSP_synth; 1.
DR PROSITE; PS50911; CHAP; 1.
KW Complete proteome.
SQ SEQUENCE 618 AA; 70240 MW; E24F56812160EC60 CRC64;

Query Match 14.1%; Score 86; DB 16; Length 618;
Best Local Similarity 29.7%; Pred. No. 0.59;
Matches 22; Conservative 20; Mismatches 26; Indels 6; Gaps 3;

QY 16 RLMAW----EKFYVLDKQKAWLP-LTETIKDRLQRLVLRREDVVLGRPM-TPTQIGPS 69
DB 439 KTWAMETAMEQIREVSEITFAVAVPIRTGPNENVRLLIDVLRPEVLEPMTVTPGKKA 498
QY 70 LPLIMQLYPDGRY 83
DB 499 ILPLMSLFPHHRY 512

RESULT 4
Q9QXN9

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ID 090XN9 PRELIMINARY; PRT; 107 AA.
AC 090XN9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE T-cell leukemia protein Tc1b3a.
GN Tc1b3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OK NCBI_TaxId=10090;
RP [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20056259; PubMed=10588720;
RA Hallas C., Bekareky Y., Itoyama T., Varnum J., Bicht R.,
RA Rothstein J.L., Croce C.M.;
RT "Genomic analysis of human and mouse Tc1b3 loci reveals a complex of
RT tightly clustered genes."
RL Proc. Natl. Acad. Sci. U.S.A. 96:14418-14423(1999).
DR EMBL; AF195491; AAF12804.1; -.
DR MGI; MGI:1351600; Tc1b3.
DR InterPro; IPR004832; Tc1b_MTCPL.
DR Pfam; PF01840; Tc1b_MTCPL; 1.
DR ProDom; PD015575; Tc1b3; 1.
SQ SEQUENCE 107 AA; 12224 MW; DDC2AAC489D02DDBE CRC64;

Query Match 13.8%; Score 84.5; DB 11; Length 107;
Best Local Similarity 23.8%; Pred. No. 0.11;
Matches 24; Conservative 22; Mismatches 54; Indels 1; Gaps 1;

QY 10 VTDFHDLTAMEKFFVYLDEKQAWLPL-TIEIKRLQLRVLRREDVVLGRPM-TPTQIGPS 69
DB 3 LSGHGLQWASLRFSGHRLQRLASLKSGLHLETG-ITVHLQMTTIPPEPFPQPINNN 61
QY 70 ILPIWMQLYPDGRYSSDSSFFRLVYHIKIDGVEMLLEL 110
DB 62 SLPTWRLFSNMTYGTGTGYRLDLDSQMGDTLQLILDI 102

RESULT 5
Q8XBW3 PRELIMINARY; PRT; 619 AA.
AC 08XBW3;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Glutathionylspermidine synthetase/amidase.
GN GSP OR Z4342 OR ECS3873.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OK NCBI_TaxId=83334;
RP [1]
RP SEQUENCE FROM N.A.
RX STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirpatrick H.A.,
RA Posel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Aanacharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RT Nature 409:529-533(2001).
RL Nature 409:529-533(2001).
RP [2]
RP SEQUENCE FROM N.A.
RX STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shingawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli

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RT O157:H7 and genomic comparison with a laboratory strain K-12."
RL DNA Res. 8:11-22(2001).
DR EMBL; AE005529; AAG58125.1; -.
DR EMBL; AP002563; BAB37296.1; -.
DR PIR; A85958; A85958.
DR PIR; A91113; A91113.
DR InterPro; IPR007921; CHAP.
DR InterPro; IPR005494; GSP_synth.
DR Pfam; PF05257; CHAP; 1.
DR Pfam; PF03738; GSP_synth; 1.
DR PROSITE; PS50911; CHAP; 1.
KW Complete proteome.
SQ SEQUENCE 619 AA; 70532 MW; 0FDB43DBA0B2933C CRC64;

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Query Match 13.6%; Score 83; DB 16; Length 619;
Best Local Similarity 28.4%; Pred. No. 1.3;
Matches 21; Conservative 21; Mismatches 26; Indels 6; Gaps 3;

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QY 16 RLWAME----KFVYLDEKQAWLPL-TIEIKRLQLRVLRREDVVLGRPM-TPTQIGPS 69
DB 440 KTWAMETAFDQIRVSDREFAVPIRTGHPQNEVRLIDVLRPEVLVPEPLTWIIPGNKA 499
QY 70 ILPIWMQLYPDGRY 83
DB 500 ILPIWLSLFPNHR 513

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RESULT 6
Q8PDM3 PRELIMINARY; PRT; 620 AA.
AC 08PDM3;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Glutathionylspermidine synthase.
GN GSP OR C3725.
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OK NCBI_TaxId=21792;
RP [1]
RP SEQUENCE FROM N.A.
RX STRAIN=O6:H1 / CFT073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesech P.,
RA Raeko D., Buckles E.L., Lion S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli";
RT Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
RL EMBL; AE016766; AAN82169.1; -.
DR InterPro; IPR007921; CHAP.
DR InterPro; IPR005494; GSP_synth.
DR Pfam; PF05257; CHAP; 1.
DR Pfam; PF03738; GSP_synth; 1.
DR PROSITE; PS50911; CHAP; 1.
KW Complete proteome.
SQ SEQUENCE 620 AA; 70623 MW; F7F0CAC273C3131B CRC64;

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Query Match 13.6%; Score 83; DB 16; Length 620;
Best Local Similarity 28.4%; Pred. No. 1.3;
Matches 21; Conservative 21; Mismatches 26; Indels 6; Gaps 3;

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QY 16 RLWAME----KFVYLDEKQAWLPL-TIEIKRLQLRVLRREDVVLGRPM-TPTQIGPS 69
DB 441 KTWAMETAFDQIRVSDREFAVPIRTGHPQNEVRLIDVLRPEVLVPEPLTWIIPGNKA 500
QY 70 ILPIWMQLYPDGRY 83
DB 501 ILPIWLSLFPNHR 514

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RC STRAIN=MOPn / Nig9;
RA MEDLINE=20150255; PubMed=10684935;
RX Read T.D., Brumham R.C., Shen C., Gail S.R., Heidelberg J.F.,
RY White O., Hickey E.K., Peterson J., Uttenback T., Berry K., Bass S.,
RA Linher K., Weidman D., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwin M., Nelson W., Deboy R., Kolony J., McClarty G., Salzberg S.L.,
RT Eisen J., Frazer C.M.;
RL "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39." ;
RL Nucleic Acids Res. 28:1397-1406(2000) .
DR EMBL; AB002337; AAF39501.1; -.
DR PIR; F81675; F81675.
DR TIGR; TC0684; -.
KM Hypothetical protein; Complete proteome.
SQ SEQUENCE 275 AA; 31234 MW; 591AB4376AB83A49 CRC64;

Query Match 12.3%; Score 75; DB 16; Length 275;
Best Local Similarity 33.7%; Pred. No. 3.9'
Matches 28; Conservative 10; Mismatches 29; Indels 16; Gaps 4

QY 39 EIKRLQLRLRRDDVTLGRPMPTQTGIPSLPLIMQLYP-----DGYRSSDS 88
DB 5 ELISGDCKKLERFDVLILRP-SATAIWPTSPALMKQSAEFVRVEKGEMKYRNHSL 63
QY 89 SFMRIVYHIKIDGVEDMLELP 111
DB 64 KEW---WTIDSV-SCLKLTP 81

RESULT 9
P73727 PRELIMINARY; PRT; 363 AA.
AC P73727;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hypothetical protein slr1737.
GN SLR1737.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chlorococcales; Synechocystis.
CX NCBI_TaxId=1148;
KN [1]
RN SEQUENCE FROM N.A.
RP MEDLIN=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hikosawa M., Sugiyura M., Sasamoto S., Kimura T.,
RA Hoanouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimpou S., Takeuchi C., Wada T., Matsuabe A., Yamada M., Tabata S.;
RA "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the RT entire genome and assignment of potential protein-coding regions."; RNA Res. 3:109-136(1996) .
RL EMBL; D90909; BAA17775.1; -.
DR PIR; S74814; S74814.
RM Hypothetical protein; Complete proteome.
SQ SEQUENCE 363 AA; 41479 MW; 992646CFDP9296D35 CRC64;

Query Match 12.1%; Score 74; DB 16; Length 363;
Best Local Similarity 25.0%; Pred. No. 7;
Matches 26; Conservative 15; Mismatches 31; Indels 32; Gaps 6;

QY 14 PDRLIAWEKFVYLDEKOHAWIPLTIEIKRIQLRVLLRRBDVVLRGPMTPT----- 64
DB 211 PSR-WFPIQANYFPD--HPGLSVTAAGER-----IVLGREBEVALIGLHQGN 256
QY 65 --QGPELSLPLIMQLYPDGRY--RSOSSSFMRIVYHIKIDGVED 104
DB 257 FYEFGPGHGTVTQVPAPWGMRQLASNDRYW----VKLSGXTD 295
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	Matches	39;	Conservative	10;	Mismatches	43;	Indels	37;	Gaps	7
Oy	10	VTD--HPDRLAMEKFEVYLD	EKHQAMLP	LPIIEIKDRLQLRVLLREEDVVLGRPMP	TQTIG	67				
		: :	:	:	:					
Dd	177	VTDGDTPTQRILYLFESLG--	DEPGEGWLGLLEIGED---	LDSWLRNDA--	GNVMILLDQH	229				
Oy	68	PSLIPIMQLYPDGRYRS-----								
		: :	:	:	:					
Dd	230	QVAVLATADAEALGSGASRTLLRGDGF	FGIAGPLPQHMYLPOHVSSSWDLIVH---	GIG	286					
Oy	104	DMLEL-LP	111							
		: :	:	:	:					
Dd	287	RLLALLMLP	295							
 RESULT 12 O58935 PRELIMINARY; PRT; 727 AA.										
AC	O58935									
DT	01-AUG-1998	(TREMBLrel. 07,	Created)							
DT	01-AUG-1998	(TREMBLrel. 07,	Last sequence update)							
DT	01-OCT-2003	(TREMBLrel. 25,	Last annotation update)							
DE	Hypothetical protein PH1246.									
GN	PH1246.									
OS	Pyrococcus horikoshii.									
OC	Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;									
CC	Pyrococcus.									
OX	NCB1_TaxID=53953;									
RN	[1]									
RP	SEQUENCE FROM N.A.									
RC	STRAIN=OTJ;									
KX	MEDLINE=98344137;	PubMed=9679194;								
FA	Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,									

RA Furukoshi T., Tanaka T., Kudon Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.,
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, *Pyrococcus horikoshii* OT3.",
RL DNA Res. 5:55-76(1998).
CC -I- SIMILARITY: TO DEAD/DEAH BOX HELICASE FAMILY.
DR EMBL: AP000005; BAA30347.1. -
DR PIR: A71069; A71069.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0008026; F:ATP dependent helicase activity; IEA.

	InterPro; IPR006483; CRISPr_HD.	
D	InterPro; IPR001410; DEAD.	
R	InterPro; IPR001650; Helicase_C.	
R	Pfam; PF00270; DEAD_1.	
R	Pfam; PF00271; helicase_C_1.	
S	SMART; SMART0487; DEXDC_1.	
O	SMART; SMART0490; HELICC_1.	
N	TIGRFAMs; TIGR01587; cas3_core_1.	
C	TIGRFAMs; TIGR01596; cas3 HD_1.	
K	ATP-binding; Helicase; Hypothetical protein; Complete proteome.	
Q	SEQUENCE 727 AA; 84768 MW; 6AAFD011AD2FEDC5 CnC64;	

	Query Match	11.7%; Score 71.5; DB 17; Length 727;
	Best Local Similarity	27.7%; Pred. No. 31;
	Matches	Conservative 13; Mismatches 42; Indels 13; Gaps 3
Qy	21 EKFFVLDKEKQAMLPETIEIKDRLOTRVLKRREDVVLRPTTPPOIGSPSLPIIMQLYPD	80
:	: :: :	:
Bb	221 EQFAEMKIPEKKRP-----IQLSSSMTEGVIL--YAPGYGKTALLWANAKNA	269
:	:: :	:
Oy	81 GRYSDDSS--FMRLTVYHIKDVGEDMDLELPP	112
:	: : :	:
Dd	270 HRTKGGISSRIEFLIPPYKASINAHRRLLLENFKD	303

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RESULT 13
O8TK58      PRELIMINARY;      PRT;      1156 AA.
AC      O8TK58;
DT      01-JUN-2002 (TREMBlrel. 21, Created)
DT      01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT      01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE      Phosphorylase.
GN      MA3560.
OS      Methanosarcina acetivorans.
OC      Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC      Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX      NCBI_TaxID=2214;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C2A / ATCC 35395 / DSM 2834;
RX      MEDLINE=21929760; PubMed=11932238;
RA      Galagan J.E., Nuebaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA      Fitzhugh W., Calvo S., Engels R., Smirnov S., Alncor D., Brown A.,
RA      Allen N., Naylor J., Stange-Thomann N., Dearellano K., Johnson R.,
RA      Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA      Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Gues A.M.,
RA      Hedderich R., Ingram-Smith C., Kuetner H.C., Krzycki J.A.,
RA      Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA      Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA      Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA      Mercalf W.W., Birren B.;
RT      "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT      and physiological diversity."
RL      Genome Res. 12:532-542(2002).
DR      EMBL; AB011064; AAM0921.1; -.
DR      GO; GO:0003824; F:catalytic activity; IEA.
DR      GO; GO:0009116; P:nucleoside metabolism; IEA.
DR      InterPro; IPR008938; ARM.
DR      InterPro; IPR00845; ENP_UDP.
DR      Pfam; PF01048; PNP_UDP_1; 1.
KW      Complete proteome.
SQ      SEQUENCE      1156 AA; 130192 MW; 0280A362DC4B5C6 CRC64;

Query Match      11.7%; Score 71.5; DB 17; Length 1156;
Best local Similarity 23.0%; Pred. No. 54;
Matches 26; Conservative 20; Mismatches 42; Indels 25; Gaps 5;

QY      6 LGFAVTDHPDRLMAWEKFFVYLDKQKAWLPLTI-----ETKDRLOQ-----RLVLLRR 52
DB      494 LGSAFSGVDPDQKQASNSIKISTBEDNMKRSAYFALGSAFSGVDPDQKQASMDIRGLTIN 553
QY      53 EDVVLGREMPTQIGPSILPLTMQLYDPGRYSSDSFRLVYHIKIDGVEDM 105
DB      554 EDSVV-RRITASLGSASFHV-----PD-----KQKAMNDLHRLSIDKEDV 594

RESULT 14
Q8VVI0      PRELIMINARY;      PRT;      380 AA.
AC      Q8VVI0;
DT      01-MAR-2002 (TREMBlrel. 20, Created)
DT      01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT      01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE      Membrane protein.
GN      CPSH.
OS      Erwinia pyrifoliae.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC      Enterobacteriaceae; Erwinia.
OX      NCBI_TaxID=79967;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Epl/96;
RC      Klm W.S.; Schollmeyer M., Nimetz M., Geider K.;
RT      "Structural and molecular properties of the capsular exopolysaccharide
RT      from the Asian pear pathogen Erwinia pyrifoliae."
RL      Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

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DR      EMBL; AJ300463; CAC82927.1; -.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:0015159; F:polysaccharide transporter activity; IEA.
DR      GO; GO:0015774; P:polysaccharide transport; IEA.
DR      InterPro; IPR003715; Poly_export.
DR      Pfam; PF02563; Poly_export; 1.
SQ      SEQUENCE      380 AA; 42023 MW; BC4C5A0A7EC66E8C CRC64;

Query Match      11.6%; Score 71; DB 2; Length 380;
Best local Similarity 24.0%; Pred. No. 16;
Matches 23; Conservative 23; Mismatches 34; Indels 16; Gaps 4;

QY      5 TLGAVTDHPDRLMAWEKFFVYLDKQKAWLPLTIETIKRLQLRVLRRREDVVLGRMPTPT 64
DB      34 TMGKDVVEQDSDPDIDKYNN-----FPLTPSLVERKRPVVAQANATLQREIQNY 86
QY      65 Q----IGPSILPLTMQ---LYPDGRYS-SDSSF 91
DB      87 EYRIGVDVLMVTVMVMDHPDLTPAGQYRSASDTGNW 122

RESULT 15
Q8VRP6      PRELIMINARY;      PRT;      363 AA.
AC      Q8VRP6;
DT      01-MAR-2002 (TREMBlrel. 20, Created)
DT      01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT      01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE      Dissimilatory sulfite reductase alpha subunit (Fragment).
GN      DSSA.
OS      Desulfocella halophila.
OC      Bacteria; Proteobacteria; Deltaproteobacteria; Desulfococcales;
OC      Desulfococcaceae; Desulfocella.
OX      NCBI_TaxID=66835;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=DSM 11763;
RX      MEDLINE=21617390; PubMed=11741869;
RA      Friedrich M.W.;
RT      "Phylogenetic Analysis Reveals Multiple Lateral Transfers of
RT      Adenosine-5'-Phosphosulfate Reductase Genes among Sulfate-Reducing
RT      Microorganisms."
RL      J. Bacteriol. 184:278-289(2002).
DR      EMBL; AF418200; AAL57473.1; -.
DR      GO; GO:0006118; P:electron transport; IEA.
DR      InterPro; IPR006067; Ntr_Str_4Fe4S.
DR      Pfam; PF01077; Ntr_Str; 1.
FT      NON_TER      1
SQ      SEQUENCE      363 AA; 41462 MW; 76D24998C7B1589A CRC64;

Query Match      11.3%; Score 69; DB 2; Length 363;
Best local Similarity 24.7%; Pred. No. 26;
Matches 22; Conservative 16; Mismatches 19; Indels 32; Gaps 4;

QY      8 EAVTDHPDRLMAWEKFFVYLDKQKAWLPLTIETIKRLQLRVLRRREDVVLGRMPTPTQIG 67
DB      282 EATIDYIDIKIMW-----WM-----MEGKRNRRGELIRQ-----G 313
QY      68 PSLLPLTMQQLYDPGRY-----RSSDSFWR 92
DB      314 PQKMLEMCEVDPDPRHVAYPRENPIYFWK 342

Search completed: June 17, 2004, 14:27:59
Job time : 67 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 17, 2004, 11:31:10 ; Search time 614 Seconds
(without alignments)
9878.440 Million cell updates/sec

Title: US-09-441-242A-1
Perfect score: 1324
Sequence: 1 ctctgagagcctcgtcctt.....catgaaaaaaaaaaaaaa 1324

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/PCTUS_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
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- 14: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1324	100.0	1324	9	US-09-796-692-665 Sequence 665, App
2	1324	100.0	1324	15	US-10-040-862-665 Sequence 225, App
3	1324	100.0	1324	15	US-10-171-581-225 Sequence 665, App
4	1324	100.0	1324	16	US-10-057-475B-665 Sequence 665, App
5	1324	100.0	1324	16	US-10-154-884B-665 Sequence 665, App
6	1280	96.7	1368	15	US-10-037-270-871 Sequence 871, App
7	1280	96.7	1368	16	US-10-117-722-871 Sequence 871, App
8	344	26.0	369	16	US-10-057-475B-10484 Sequence 10484, A
9	344	26.0	369	16	US-10-154-884B-10484 Sequence 10484, A
10	285	21.5	285	9	US-09-796-692-321 Sequence 321, App
11	285	21.5	285	9	US-09-796-692-468 Sequence 468, App
12	285	21.5	285	9	US-09-796-692-3032 Sequence 3032, App
13	285	21.5	285	9	US-09-796-692-5832 Sequence 5832, App
14	285	21.5	285	9	US-09-796-692-6894 Sequence 6894, App

C 15	285	21.5	285	15	US-10-040-862-321	Sequence 321, App
C 16	285	21.5	285	15	US-10-040-862-468	Sequence 468, App
C 17	285	21.5	285	15	US-10-040-862-3032	Sequence 3032, App
C 18	285	21.5	285	15	US-10-040-862-5832	Sequence 5832, App
C 19	285	21.5	285	15	US-10-040-862-6894	Sequence 6894, App
C 20	285	21.5	285	16	US-10-057-475B-321	Sequence 321, App
C 21	285	21.5	285	16	US-10-057-475B-468	Sequence 468, App
C 22	285	21.5	285	16	US-10-057-475B-3032	Sequence 3032, App
C 23	285	21.5	285	16	US-10-057-475B-5832	Sequence 5832, App
C 24	285	21.5	285	16	US-10-057-475B-6894	Sequence 6894, App
C 25	285	21.5	285	16	US-10-154-884B-321	Sequence 321, App
C 26	285	21.5	285	16	US-10-154-884B-468	Sequence 468, App
C 27	285	21.5	285	16	US-10-154-884B-3032	Sequence 3032, App
C 28	285	21.5	285	16	US-10-154-884B-5832	Sequence 5832, App
C 29	285	21.5	285	16	US-10-154-884B-6894	Sequence 6894, App
C 30	284.4	21.5	290	9	US-09-796-692-6197	Sequence 6197, App
C 31	284.4	21.5	290	15	US-10-040-862-6197	Sequence 6197, App
C 32	284.4	21.5	290	16	US-10-057-475B-6197	Sequence 6197, App
C 33	284.4	21.5	290	16	US-10-154-884B-6197	Sequence 6197, App
C 34	283.4	21.4	285	9	US-09-796-692-418	Sequence 418, App
C 35	283.4	21.4	285	9	US-09-796-692-518	Sequence 518, App
C 36	283.4	21.4	285	9	US-09-796-692-6556	Sequence 6556, App
C 37	283.4	21.4	285	15	US-10-040-862-6556	Sequence 6556, App
C 38	283.4	21.4	285	15	US-10-040-862-518	Sequence 518, App
C 39	283.4	21.4	285	15	US-10-040-862-6556	Sequence 6556, App
C 40	283.4	21.4	285	16	US-10-057-475B-418	Sequence 418, App
C 41	283.4	21.4	285	16	US-10-057-475B-518	Sequence 518, App
C 42	283.4	21.4	285	16	US-10-057-475B-6556	Sequence 6556, App
C 43	283.4	21.4	285	16	US-10-154-884B-418	Sequence 418, App
C 44	283.4	21.4	285	16	US-10-154-884B-518	Sequence 518, App
C 45	283.4	21.4	285	16	US-10-154-884B-6556	Sequence 6556, App

ALIGNMENTS

RESULT 1
US-09-796-692-665
Sequence 665, Application US/09796692
Publication No. US20020196362A1
GENERAL INFORMATION:
APPLICANT: Galger, Alexander
APPLICANT: Algaier, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
FILE REFERENCE: 2077, 001200
CURRENT APPLICATION NUMBER: 60/09796, 692
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186, 126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/190, 479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/200, 545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/200, 303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200, 779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200, 999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/202, 084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/206, 201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: 60/218, 950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/222, 903
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 60/223, 416
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: 60/223, 378
PRIOR FILING DATE: 2000-08-07

NUMBER OF SEQ ID NOS: 9597
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 665
LENGTH: 1324
TYPE: DNA
ORGANISM: Homo sapiens
US-09-796-692-665

Query Match 100.0%; Score 1324; DB 9; Length 1324;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 ACACCTGGGGAGGAGCTCAACCGACCCGAGCCGCTGTGGGCTGGAGAGTTCTGTG 120
QY 121 TATTGGAAGAGACAGACAGCCCTGCTGCTTAAACATCGAGATTAAGATAGTTA 180
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DB 181 CAGTTACGGGCTCTTCTGCTGCGGAGACGTCCTGTGGGAGGCTATGACCCCAAC 240
QY 241 CAGATAGGCCCAAGCTGCTGCTATCATGTGGAGCTCTACCTGATGACGATACCGA 300
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DB 781 CAGCCGATTAACCTGAGACAGACCTCTGAAACCTTGACCAAGTGTCTCAATGTGCTA 840
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DB 841 CGCCTGATGAAACAGCCTGCAAAAGCTGCTGCGGTAAACAGCCTGCAAAAGCCTG 900
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QY 1021 CCACATCCCGGAGCGCAGCAGAGCCGAGCCGAGCCCTGTGATGAGCCCTCAGAA 1080
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QY 1081 CCCTGGCTGGCCACGCTGGAAGAGATGAGGTTGGTTTCCCTTATAGATGCT 1140
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QY 1321 AAAA 1324
DB 1321 AAAA 1324
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RESULT 2
US-10-040-862-665
Sequence 665, Application US/10040862
Publication No. US20030078396A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Maignon, Jane
APPLICANT: Retter, Marc
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
FILE REFERENCE: 014058-013520US
CURRENT APPLICATION NUMBER: US/10/040,862
PRIOR FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/223,416
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: US 60/223,378
PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: US 09/796,692
PRIOR FILING DATE: 2001-03-01

NUMBER OF SEQ ID NOS: 10467
SOFTWARE: PaedSeq for Windows Version 3.0
SEQ ID NO: 665
LENGTH: 1324
TYPE: DNA
ORGANISM: Homo sapiens
US-10-040-862-665

Query Match 100.0%; Score 1324; DB 15; Length 1324;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 ACACCTGGGAGGAGGAGTCAACCGAGCCGAGCCGCTGTGGGCTGTGGAGAGTTGCTG 120
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DB 841 CGCTGCTATGTAACAGCGCTGCAAGCGCTGCTGCGGTAAACAGCGCTGCAAGCGCTG 900
QY 901 CCGTGCCTGTAACAGCGCTGCAAGCGCTGCTGCGGTAAACAGCGCTGCAAGCGCTG 960
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DB 1021 CCACATCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080
QY 1081 CCGTTGCTGCTGCGCAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1140
DB 1081 CCGTTGCTGCTGCGCAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1140
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DB 1201 AATGCAAGATGATTATCTAATCTGTCGCGCAATCAGCTTATCCTTGAATGATTTCT 1260
QY 1261 GGTGAGAGAGTGAAGATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320
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QY 1321 AAAA 1324
DB 1321 AAAA 1324
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RESULT 3
US-10-171-581-225
Sequence 225, Application US/10171581
Publication No. US20030104426A1
GENERAL INFORMATION:
APPLICANT: Dai, Hongyue
APPLICANT: Linsley, Peter
TITLE OF INVENTION: Signature Genes in Chronic Myelogenous Leukemia
FILE REFERENCE: 9301-157-999
CURRENT APPLICATION NUMBER: US/10/171,581
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 60/298,914
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 366
SEQ ID NO 225
LENGTH: 1324
TYPE: DNA
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: X82240
DATABASE ENTRY DATE: 2001-06-18
US-10-171-581-225

Query Match 100.0%; Score 1324; DB 15; Length 1324;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CTTGAGAGGCTCTGCTCTTCTTTAGGCGCCGAGAGAGCCATGAGCCGAGTGGCCG 60
QY 61 ACACCTGGGAGGAGGAGTCAACCGAGCCGAGCCGCTGTGGGCTGTGGAGAGTTGCTG 120
DB 61 ACACCTGGGAGGAGGAGTCAACCGAGCCGAGCCGCTGTGGGCTGTGGAGAGTTGCTG 120
QY 121 TATTGGACGAGAGACGACGCGCTGCTTAAACATGAGATTAAGATAGTTA 180
DB 121 TATTGGACGAGAGACGACGCGCTGCTTAAACATGAGATTAAGATAGTTA 180
QY 181 CAGTTACGGGAGTCTTGTGCGGAGAGAGTCTGCTGGGAGAGGCTATGAGACCCGACC 240
DB 181 CAGTTACGGGAGTCTTGTGCGGAGAGAGTCTGCTGGGAGAGGCTATGAGACCCGACC 240
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[illegible]

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Db	1321	AAAA 1324	
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		RESULT 4	
		US-10-057-475B-665	
		/ Sequence 665, Application US/10057475B	
		/ Publication No. US20040002068A1	
		/ GENERAL INFORMATION:	
		/ APPLICANT: Gaiger, Alexander	
		/ APPLICANT: Algste, Paul A.	
		/ APPLICANT: Mannion, Jane	
		/ APPLICANT: Clapper, Jonathan David	
		/ APPLICANT: Wang, Aijun	
		/ APPLICANT: Ordonez, Nadia	
		/ APPLICANT: Carter, Lauren	
		/ APPLICANT: McNeill, Patricia Dianne	
		/ TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and	
		/ FILE REFERENCE: 014058-014402US	
		/ CURRENT APPLICATION NUMBER: US/10/057, 475B	
		/ CURRENT FILING DATE: 2002-01-22	
		/ PRIOR APPLICATION NUMBER: US 60/166,126	
		/ PRIOR FILING DATE: 2000-03-01	
		/ PRIOR APPLICATION NUMBER: US 60/190,479	
		/ PRIOR FILING DATE: 2000-03-17	
		/ PRIOR APPLICATION NUMBER: US 60/200,545	
		/ PRIOR FILING DATE: 2000-04-27	
		/ PRIOR APPLICATION NUMBER: US 60/200,303	
		/ PRIOR FILING DATE: 2000-04-28	
		/ PRIOR APPLICATION NUMBER: US 60/200,779	
		/ PRIOR FILING DATE: 2000-04-28	
		/ PRIOR APPLICATION NUMBER: US 60/200,999	
		/ PRIOR FILING DATE: 2000-05-01	
		/ PRIOR APPLICATION NUMBER: US 60/202,084	
		/ PRIOR FILING DATE: 2000-05-04	
		/ PRIOR APPLICATION NUMBER: US 60/206,201	
		/ PRIOR FILING DATE: 2000-05-22	
		/ PRIOR APPLICATION NUMBER: US 60/218,950	
		/ PRIOR FILING DATE: 2000-07-14	
		/ PRIOR APPLICATION NUMBER: US 60/222,903	
		/ PRIOR FILING DATE: 2000-08-03	
		/ Remaining Prior Application data removed - See File Wrapper or PALM.	
		/ NUMBER OF SEQ ID NOS: 10979	
		/ SOFTWARE: FastSeq for Windows Version 3.0	
		/ SEQ ID NO 665	
		/ LENGTH: 1324	
		/ TYPE: DNA	
		/ ORGANISM: Homo sapiens	
		/ US-10-057-475B-665	
		Query Match 100.0%; Score 1324; DB 16; Length 1324;	
		Best Local Similarity 100.0%; Pred. No. 0;	
		Matches 1324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	CTTGAGAGGCTCTGGGCTCTTGGCTTTAGAGGCGCCGAGAGAGCCATGGCCGAGTGGCCG 60	
Db	1	CTTGAGAGGCTCTGGGCTCTTGGCTTTAGAGGCGCCGAGAGAGCCATGGCCGAGTGGCCG 60	
QY	61	ACACTCGGGAGGCACTGCAACGACCAACCGGACCGGCTGTGGGCTTGGAGAGATTGCTG 120	
Db	61	ACACTCGGGAGGCACTGCAACGACCAACCGGACCGGCTGTGGGCTTGGAGAGATTGCTG 120	
QY	121	TATTTGACGAGAGACGACGCTTGGCTGCGCTTTAACATGAGATTAAAGATTGTTA 180	
Db	121	TATTTGACGAGAGACGACGCTTGGCTGCGCTTTAACATGAGATTAAAGATTGTTA 180	
QY	181	CAATTACGGGTGCTCTTGGCTGCGGAGACGTCGTCCTGGGAGGCTTATGACCCCAAC 240	

Db 181 CAGTTACGGGTCCTTGGCTGGGAGACGTGTCCTGGGAGGCTTATGACCCCAACC 240
 Qy 241 CAGATTAGGCCAAGCCTGCTGCTATCATGTGGAGAGCTTACCTGATGAGATACCGA 300
 Db 241 CAGATTAGGCCAAGCCTGCTGCTATCATGTGGAGAGCTTACCTGATGAGATACCGA 300
 Qy 301 TCCCTAGACTCCAGATTTCTGGGCTTATGTATCACAATCAATGATGAGAGGAGAC 360
 Db 301 TCCCTAGACTCCAGATTTCTGGGCTTATGTATCACAATCAATGATGAGAGGAGAC 360
 Qy 361 ATGCTTCTGAGAGCTGCTGCAATGATGATGATGATGATGATGATGATGATGATGAT 420
 Db 361 ATGCTTCTGAGAGCTGCTGCAATGATGATGATGATGATGATGATGATGATGATGAT 420
 Qy 421 CACCCAGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 480
 Db 421 CACCCAGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 480
 Qy 481 GTTTACTATGCTGTGTCTTCTCACAACAGCTGGGGTCTGGGAGGATGAGACAGACAG 540
 Db 481 GTTTACTATGCTGTGTCTTCTCACAACAGCTGGGGTCTGGGAGGATGAGACAGACAG 540
 Qy 541 GATGAGCTTACCCAGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 600
 Db 541 GATGAGCTTACCCAGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 600
 Qy 601 TACCACTCCTGCAAGAGGATTCATTGGAGAGCTTCTTCAGAGGCTGAGGCTGAGGCTGAG 660
 Db 601 TACCACTCCTGCAAGAGGATTCATTGGAGAGCTTCTTCAGAGGCTGAGGCTGAGGCTGAG 660
 Qy 661 CTGTGCTGCTGCTTCTTCTGAGTGTGCTTCTGAGCTTCTTCTGCTTCTGCTTCTGCT 720
 Db 661 CTGTGCTGCTGCTTCTTCTGAGTGTGCTTCTGAGCTTCTTCTGCTTCTGCTTCTGCT 720
 Qy 721 CCTCAAGCACTAGTATTTCTGTCACACCCACTGAGCTTCTGCTGCTGCTGCTGCTGCTG 780
 Db 721 CCTCAAGCACTAGTATTTCTGTCACACCCACTGAGCTTCTGCTGCTGCTGCTGCTGCTG 780
 Qy 781 CAGCCGATTCAGCTGAGAGGACCTTGTAAACCTTGTAGACCAATGCTTCAATGTGTCTA 840
 Db 781 CAGCCGATTCAGCTGAGAGGACCTTGTAAACCTTGTAGACCAATGCTTCAATGTGTCTA 840
 Qy 841 CGCCTGATGTAAACAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
 Db 841 CGCCTGATGTAAACAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
 Qy 901 CCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
 Db 901 CCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
 Qy 961 GAAAGGCTGAAAGAGGCTTATCTGTGCTGAGACTCAGAAAGCTTGGGCTGAGTGTGT 1020
 Db 961 GAAAGGCTGAAAGAGGCTTATCTGTGCTGAGACTCAGAAAGCTTGGGCTGAGTGTGT 1020
 Qy 1021 CCACATCCCGGAGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080
 Db 1021 CCACATCCCGGAGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080
 Qy 1081 CCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
 Db 1081 CCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
 Qy 1141 CACGCACTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
 Db 1141 CACGCACTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
 Qy 1201 AATGCAAGTATGTTATCTTAACTTGTGCTGAGTACGCTTCTGCTGCTGCTGCTGCTGCTG 1260
 Db 1201 AATGCAAGTATGTTATCTTAACTTGTGCTGAGTACGCTTCTGCTGCTGCTGCTGCTGCTG 1260
 Qy 1261 GGTGAGAGAGTGAATGAGTGGCAGGCCCAATATATATGATGAGAAAAA 1320
 Db 1261 GGTGAGAGAGTGAATGAGTGGCAGGCCCAATATATATGATGAGAAAAA 1320

Qy 1321 AAAA 1324
 Db 1321 AAAA 1324
 RESULT 5
 US-10-154-884B-665
 ; Sequence 665, Application US/10154884B
 ; Publication No. US2004000561A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Galger, Alexander
 ; APPLICANT: Algate, Paul A.
 ; APPLICANT: Mannion, Jane
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Corixa Corporation
 ; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
 ; FILE REFERENCE: 014058-013521US
 ; CURRENT APPLICATION NUMBER: US/10/154,884B
 ; CURRENT FILING DATE: 2002-05-23
 ; PRIOR APPLICATION NUMBER: US 60/186,126
 ; PRIOR FILING DATE: 2000-03-01
 ; PRIOR APPLICATION NUMBER: US 60/190,479
 ; PRIOR FILING DATE: 2000-03-17
 ; PRIOR APPLICATION NUMBER: US 60/200,545
 ; PRIOR FILING DATE: 2000-04-27
 ; PRIOR APPLICATION NUMBER: US 60/200,303
 ; PRIOR FILING DATE: 2000-04-28
 ; PRIOR APPLICATION NUMBER: US 60/200,779
 ; PRIOR FILING DATE: 2000-04-28
 ; PRIOR APPLICATION NUMBER: US 60/200,999
 ; PRIOR FILING DATE: 2000-05-01
 ; PRIOR APPLICATION NUMBER: US 60/202,084
 ; PRIOR FILING DATE: 2000-05-04
 ; PRIOR APPLICATION NUMBER: US 60/206,201
 ; PRIOR FILING DATE: 2000-05-22
 ; PRIOR APPLICATION NUMBER: US 60/218,950
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: US 60/222,903
 ; PRIOR FILING DATE: 2000-08-03
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 11290
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 665
 ; LENGTH: 1324
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-154-884B-665
 Query Match 100.0%; Score 1324; DB 16; Length 1324;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CTTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
 Db 1 CTTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
 Qy 61 ACACCTGGGAGGAGCAGTACCGACCAACCGGACCGCTGTGGGCTGGGAGAGTTGCTG 120
 Db 61 ACACCTGGGAGGAGCAGTACCGACCAACCGGACCGCTGTGGGCTGGGAGAGTTGCTG 120
 Qy 121 TATTTGAGCGAGAGCAGACAGCCTGCTGCTGCTTAAACATCGAGATTAAGGATGCTTA 180
 Db 121 TATTTGAGCGAGAGCAGACAGCCTGCTGCTGCTTAAACATCGAGATTAAGGATGCTTA 180
 Qy 181 CAGTTAGCGGAGCTCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 Db 181 CAGTTAGCGGAGCTCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 Qy 241 CAGATTAGGCCAAGCCTGCTGCTATCATGTGGAGTCTTACCTGATGAGCGATACCGA 300
 Db 241 CAGATTAGGCCAAGCCTGCTGCTATCATGTGGAGTCTTACCTGATGAGCGATACCGA 300

Qy	301	TCCTCAGACTCCAGTTTCTGGCGCTTAGTGTACCAATCAAGATTGACGGCGTGGAGAC	360
Db	301	TCCTCAGACTCCAGTTTCTGGCGCTTAGTGTACCAATCAAGATTGACGGCGTGGAGAC	360
Qy	361	ATGCTTCGAGCTGCTGCCAGATGATGTAGTATGGTCTTGGGAGACCTGTCCTTT	420
Db	361	ATGCTTCGAGCTGCTGCCAGATGATGTATGGTCTTGGGAGACCTGTCCTTT	420
Qy	421	CACCCAGGGGCTGAGCCTGGCCAGCCTCAATGGGGATGTGTGTTCTGTTCACTTC	480
Db	421	CACCCAGGGGCTGAGCCTGGCCAGCCTCAATGGGGATGTGTGTTCTGTTCACTTC	480
Qy	481	GTTTACTATGCTGTGTCTTCTCCACACACCTGGGGCTGTGGAGAAATGACAGACAG	540
Db	481	GTTTACTATGCTGTGTCTTCTCCACACACCTGGGGCTGTGGAGAAATGACAGACAG	540
Qy	541	GATGAGCTTACCCAGGGGCTGCAGAGACCTGCTGTAGCCCACTGTGCTGAGCTTGGAC	600
Db	541	GATGAGCTTACCCAGGGGCTGCAGAGACCTGCTGTAGCCCACTGTGCTGAGCTTGGAC	600
Qy	601	TACCACTCCCTGCAAGAGAGATTCATTTGGCAGAGCTTCTTCAAGTGGCCAGCTAAC	660
Db	601	TACCACTCCCTGCAAGAGAGATTCATTTGGCAGAGCTTCTTCAAGTGGCCAGCTAAC	660
Qy	661	CTGTGCTCGGCTTTTCTCAGCTGAGTATGAGCTTCAAGCTCTTCTGTGCTGCTGTGC	720
Db	661	CTGTGCTCGGCTTTTCTCAGCTGAGTATGAGCTTCTTCAAGCTCTTCTGTGCTGCTGTGC	720
Qy	721	CTCTCAGACACTGTATTTCTATGTTGCACACCACTCAGCTCCGTGAACCTGTGAGAAC	780
Db	721	CTCTCAGACACTGTATTTCTATGTTGCACACCACTCAGCTCCGTGAACCTGTGAGAAC	780
Qy	781	CAGCCGATTCACCTGAGCAGGACCTGTGAACCTGTGACACATGGTCTCAATGGTGCTA	840
Db	781	CAGCCGATTCACCTGAGCAGGACCTGTGAACCTGTGACACATGGTCTCAATGGTGCTA	840
Qy	841	CGCTGCATGTAAACA CGGCTGTGAACCGCTGCTGCCTGGTGAACAAGCCTGCAGAAAGCTG	900
Db	841	CGCTGCATGTAAACA CGGCTGTGAACCGCTGCTGCCTGGTGAACAAGCCTGCAGAAAGCTG	900
Qy	901	CCGTGCCGTAAACAGCCCTGCAACAGCTGCTGCCCCACACAGGTTCAAGTGCAGCTCAAG	960
Db	901	CCGTGCCGTAAACAGCCCTGCAACAGCTGCTGCCCCACACAGGTTCAAGTGCAGCTCAAG	960
Qy	961	GAAAGGCTGAAAGAGGCCCTTATCTGTGCTCAGGACTCAGAAAGGCTGTGGGTCAAGTGT	1020
Db	961	GAAAGGCTGAAAGAGGCCCTTATCTGTGCTCAGGACTCAGAAAGGCTGTGGGTCAAGTGT	1020
Qy	1021	CCACATCCCGGAGACGACAGAGAGGCGCGGAGAGCCCTGTGGATGAGCCCTCAGAA	1080
Db	1021	CCACATCCCGGAGACGACAGAGAGGCGCGGAGAGCCCTGTGGATGAGCCCTCAGAA	1080
Qy	1081	CCCTTGGCTTGGCCAGGTGGAAGAGATGAGGTTGGTTCCCCCTTTATAGATGT	1140
Db	1081	CCCTTGGCTTGGCCAGGTGGAAGAGATGAGGTTGGTTCCCCCTTTATAGATGT	1140
Qy	1141	CAGCAGCCTGGGTGTAAACAAATTGTATGTGGCATTACTTTTGTAAATGATTGATTA	1200
Db	1141	CAGCAGCCTGGGTGTAAACAAATTGTATGTGGCATTACTTTTGTAAATGATTGATTA	1200
Qy	1201	AATGCAATATGTTATCTAACTTGTGTGCGCAATAGCTTCTATCTTGAAGTTGATTC	1260
Db	1201	AATGCAATATGTTATCTAACTTGTGTGCGCAATAGCTTCTATCTTGAAGTTGATTC	1260
Qy	1261	GGTGGAGAGATGAGATAGGACGCCCAATTTAAATTAATTCATGAGAAAAAATAA	1320
Db	1261	GGTGGAGAGATGAGATAGGACGCCCAATTTAAATTAATTCATGAGAAAAAATAA	1320
Qy	1321	AAAA 1324	
Db	1321	AAAA 1324	

	RESULT 6	
	US-10-037-270-871	
/	Sequence 871, Application US/10037270	
/	Publication No. US20030104529A1	
/	GENERAL INFORMATION:	
/	APPLICANT: Tang, Y. Tom	
/	APPLICANT: Liu, Chenghua	
/	APPLICANT: Asundi, Vinod	
/	APPLICANT: Zhang, Jie	
/	APPLICANT: Ren, Feiyang	
/	APPLICANT: Chen, Rui-hong	
/	APPLICANT: Zhao, Qing A.	
/	APPLICANT: Wehrman, Tom	
/	APPLICANT: Xue, Aidong J.	
/	APPLICANT: Yang, Yongshong	
/	APPLICANT: Wang, Jian-Rui	
/	APPLICANT: Zhou, Ping	
/	APPLICANT: Ma, Yunqing	
/	APPLICANT: Wang, Dunrui	
/	APPLICANT: Wang, Zhiwei	
/	APPLICANT: Tillinghast, John	
/	APPLICANT: Drmanac, Radoje T.	
/	TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and	
/	FILE REFERENCE: Polypeptides	
/	CURRENT APPLICATION NUMBER: US/10/037,270	
/	PRIOR FILING DATE: 2002-01-04	
/	PRIOR APPLICATION NUMBER: 09/552,317	
/	PRIOR FILING DATE: 2000-04-25	
/	PRIOR APPLICATION NUMBER: 09/488,725	
/	PRIOR FILING DATE: 2000-01-21	
/	NUMBER OF SEQ ID NOS: 1104	
/	SOFTWARE: pf_Fl_genes Version 1.0	
/	SEQ ID NO 871	
/	LENGTH: 1368	
/	TYPE: DNA	
/	ORGANISM: Homo sapiens	
/	FEATURE:	
/	NAME/KEY: CDS	
/	LOCATION: (103)..(447)	
/	US-10-037-270-871	
Query Match	96.7%; Score 1280; DB 15; Length 1368;	
Best Local Similarity	99.8%; Pred. No. 0;	
Matches 1302; Conservative	0; Mismatches 0; Indels 2; Gaps 2	
Dy	8 GGCTGTGGCTTTGCTTCTTAGCGGGCCGAGACGCCATGCGAGTGCCCGACACTCG	67
Dd	65 GGCTGTGGCTTTGCTTCTTAGCGGGCCGAGACGCCATGCGAGTGCCCGACACTCG	124
Dy	68 GGAAGCAGTCACCGACCAACCAGACCGCTGTGGGCTGTGGAGAAGTGTGTAATTGG	127
Dd	125 GGAAGCAGTCACCGACCAACCAGACCGCTGTGGGCTGTGGAGAAGTGTGTAATTGG	184
Dy	128 ACCAGAACGACACAGCTGCTGGCTGCCTTAAACATCGAGATAAAGATAGTTACAGTTAC	187
Dd	185 ACCAGAACGACACAGCTGCTGGCTGCCTTAAACATCGAGATAAAGATAGTTACAGTTAC	244
Dy	188 GGGTGTCTTGGCGTCGGAAGACGTCGTCCTGGGAGAGCCATATACCCCAACAAGTAG	247
Dd	245 GGGTGTCTTGGCGTCGGAAGACGTCGTCCTGGGAGAGCCATATATACCCCAACAAGTAG	304
Dy	248 GCCCAAGCTGTGCTCATCATGTGGAGCTTACCTCTATGACGATACCGATCTCAG	307
Dd	305 GCCCAAGCTGTGCTCATCATGTGGAGCTTACCTCTATGACGATACCGATCTCAG	364
Dy	308 ACTCCAGTTTCTGACGCTTAGTATCCACATCAAAGATGACGGCTGAGAGACATGCTTC	367
Dd	365 ACTCCAGTTTCTGACGCTTAGTATCCACATCAAAGATGACGGCTGAGAGACATGCTTC	424
Dy	368 TCAGCTGTGCTGCCAGATGACTGATGTATGGTCTTGGCAGCACCTGTCTCTCTTACCCCCA	427


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Qy 727 AGACATGATTTTCATGTTGACACCCACTGAGTCCGTGAACCTTGAGAAACAGCCG 786
Dy 785 AGCACTGATTTTATGTTGACACCCACTGAGTCCGTGAACCTTGAGAAACAGCCG 844
Qy 787 ATTCACCTGACAGACCTCTGAAACCTTGACAGTGTCTCATGTGTCTACGCGCTG 846
Dy 845 ATTCACCTGACAGACCTCTGAAACCTTGACAGTGTCTCATGTGTCTACGCGCTG 904
Qy 847 CATTTAAACAGCCTTGCAAAAGCTGCTGCGGTAAACAGCCTTGCAAAAGCTGCTG 906
Dy 905 CATTTAAACAGCCTTGCAAAAGCTGCTGCGGTAAACAGCCTTGCAAAAGCTGCTG 964
Qy 907 CGTAAACAGCCTTGCAAAAGCTGCTGCGGTAAACAGCCTTGCAAAAGCTGCTG 966
Dy 965 CGTAAACAGCCTTGCAAAAGCTGCTGCGGTAAACAGCCTTGCAAAAGCTGCTG 1024
Qy 967 CTTGAAAGAGACCTTATCTGTGCTCAGACTCAGAAAGCTCTGAGTCAAGTCTCAAT 1026
Dy 1025 CTTGAAAGAGACCTTATCTGTGCTCAGACTCAGAAAGCTCTGAGTCAAGTCTCAAT 1084
Qy 1027 CCGCGGACGACGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1086
Dy 1085 CCGCGGACGACGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1144
Qy 1087 GCTTGCCCAAGTGAAGGATGAGGTTGGGTTTCCCGCC-TTTATGATGTCACGC 1145
Dy 1145 GCTTGCCCAAGTGAAGGATGAGGTTGGGTTTCCCGCC-TTTATGATGTCACGC 1204
Qy 1146 ACCTGGGTGTTCAAGTGTGATGTGCGATGATCTTTTGTATGATGATTTAAATGC 1205
Dy 1205 ACCTGGGTGTTCAAGTGTGATGTGCGATGATCTTTTGTATGATGATTTAAATGC 1264
Qy 1206 AAGTATGTTTATCTTAATCTTGTGCGCAATGAGCTTTTATCTTGAATTAATTTCTGTG 1265
Dy 1265 AAGTATGTTTATCTTAATCTTGTGCGCAATGAGCTTTTATCTTGAATTAATTTCTGTG 1324
Qy 1266 AGAAGAGTGAATAGGACGCGCCCAATTAATAATTTTCATGG 1309
Dy 1325 AGAAGAGTGAATAGGACGCGCCCAATTAATAATTTTCATGG 1368

RESULT 8
US-10-057-475B-10484
; Sequence 10484, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aljun
; APPLICANT: Ordenez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
```

```
;; PRIOR APPLICATION NUMBER: US 60/202,084
;; PRIOR FILING DATE: 2000-05-04
;; PRIOR APPLICATION NUMBER: US 60/206,201
;; PRIOR FILING DATE: 2000-05-22
;; PRIOR APPLICATION NUMBER: US 60/218,950
;; PRIOR FILING DATE: 2000-07-14
;; PRIOR APPLICATION NUMBER: US 60/222,303
;; PRIOR FILING DATE: 2000-08-03
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 10979
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 10484
;; LENGTH: 369
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: His-TCL-1, TCL-1 with His tag
US-10-057-475B-10484
Query Match 26.0%; Score 344; DB 16; Length 369;
Best Local Similarity 100.0%; Pred. No. 1.6e-100;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 49 GCGAGTGCCTGACACTCGGAGAGGAGTCACCGACCCGACCGCTGTGGGCTTG 108
Dy 25 GCGAGTGCCTGACACTCGGAGAGGAGTCACCGACCCGACCGCTGTGGGCTTG 84
Qy 109 GAGAGCTCTGTATTTTGGACGGAAGCAGCAGCCTGCTGCTTAAACATCGAGATA 168
Dy 85 GAGAGCTCTGTATTTTGGACGGAAGCAGCAGCCTGCTGCTTAAACATCGAGATA 144
Qy 169 AAGATAGTTACAGTTACGGGTGCTCTTGCCTGGGAAAGCTGCTGTGGAGGCTT 228
Dy 145 AAGATAGTTACAGTTACGGGTGCTCTTGCCTGGGAAAGCTGCTGTGGAGGCTT 204
Qy 229 ATGACCCCAACCAAGATAGGCGCAAGCTGCTCTTATCATGTGGAGCTTACCTGAT 288
Dy 205 ATGACCCCAACCAAGATAGGCGCAAGCTGCTCTTATCATGTGGAGCTTACCTGAT 264
Qy 289 GAGCGATACCGATCTCCAGCTCAGCTTCTGCGGCTTGTGTACCATCAAGATTGAC 348
Dy 265 GAGCGATACCGATCTCCAGCTCAGCTTCTGCGGCTTGTGTACCATCAAGATTGAC 324
Qy 349 GCGGTGAGGACATGCTTCTGAGCTGCTGCCAGATGACTGATG 392
Dy 325 GCGGTGAGGACATGCTTCTGAGCTGCTGCCAGATGACTGATG 368

RESULT 9
US-10-154-884B-10484
; Sequence 10484, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
```

;; PRIOR APPLICATION NUMBER: US 60/200,999
;; PRIOR FILING DATE: 2000-05-01
;; PRIOR APPLICATION NUMBER: US 60/202,084
;; PRIOR FILING DATE: 2000-05-04
;; PRIOR APPLICATION NUMBER: US 60/206,201
;; PRIOR FILING DATE: 2000-05-22
;; PRIOR APPLICATION NUMBER: US 60/218,950
;; PRIOR FILING DATE: 2000-07-14
;; PRIOR APPLICATION NUMBER: US 60/222,903
;; PRIOR FILING DATE: 2000-08-03
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 11290
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 10484
;; LENGTH: 369
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: His-TCL-1, TCL-1 with His tag
US-10-154-884B-10484

Query Match 25.0%; Score 344; DB 16; Length 369;

Best Local Similarity 100.0%; Pred. No. 1,6e-100; Indels 0; Gaps 0;

Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 49 GCCGAGTCCCGACACTCGGGAGGAGGAGTCAACCCGAGCCGCGCTGTGGGCTGG 108
Db 25 GCCGAGTCCCGACACTCGGGAGGAGGAGTCAACCCGAGCCGCGCTGTGGGCTGG 84
Qy 109 GAGAAATTGCTGATTTTGGACGAGAGAGCAGCGCTGCGCTTAAACATCGAGATA 168
Db 85 GAGAAATTGCTGATTTTGGACGAGAGAGCAGCGCTGCGCTTAAACATCGAGATA 144
Qy 169 AAGATAGATTACATTACGGGTGCTTTGGCTCGGGAAAGAGCTGCTTGGGGAGGCTT 228
Db 145 AAGATAGATTACATTACGGGTGCTTTGGCTCGGGAAAGAGCTGCTTGGGGAGGCTT 204
Qy 229 ATGACCCCGACAGATAGGCGCAAGCCGCTGCTTATCATGTGAGCAGTCAACCTGAT 288
Db 205 ATGACCCCGACAGATAGGCGCAAGCCGCTGCTTATCATGTGAGCAGTCAACCTGAT 264
Qy 289 GAGCAGATCCGATCTCCAGACTCCAGTTTCTGCGCTTAGTGTACACATCAAGATTGAC 348
Db 265 GAGCAGATCCGATCTCCAGACTCCAGTTTCTGCGCTTAGTGTACACATCAAGATTGAC 324
Qy 349 GGCGTGGAGACATGCTTCTCGAGCTGCTGCCAGATGACTGATG 392
Db 325 GGCGTGGAGACATGCTTCTCGAGCTGCTGCCAGATGACTGATG 368

RESULT 10

US-09-796-692-321/c
;; Sequence 321, Application US/09796692
;; Publication No. US20020198362a1
;; GENERAL INFORMATION:
;; APPLICANT: Gaiger, Alexander
;; APPLICANT: Algate, Paul A.
;; APPLICANT: Mannion, Jane
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
;; FILE REFERENCE: 2077.001200
;; CURRENT APPLICATION NUMBER: US/09/796,692
;; PRIOR APPLICATION NUMBER: 2001-03-01
;; PRIOR FILING DATE: 2000-03-01
;; PRIOR APPLICATION NUMBER: 60/190,479
;; PRIOR FILING DATE: 2000-03-17
;; PRIOR APPLICATION NUMBER: 60/200,545
;; PRIOR FILING DATE: 2000-04-27
;; PRIOR APPLICATION NUMBER: 60/200,303
;; PRIOR FILING DATE: 2000-04-28
;; PRIOR APPLICATION NUMBER: 60/200,779
;; PRIOR FILING DATE: 2000-04-28

;; PRIOR APPLICATION NUMBER: 60/200,999
;; PRIOR FILING DATE: 2000-05-01
;; PRIOR APPLICATION NUMBER: 60/202,084
;; PRIOR FILING DATE: 2000-05-04
;; PRIOR APPLICATION NUMBER: 60/206,201
;; PRIOR FILING DATE: 2000-05-22
;; PRIOR APPLICATION NUMBER: 60/218,950
;; PRIOR FILING DATE: 2000-07-14
;; PRIOR APPLICATION NUMBER: 60/222,903
;; PRIOR FILING DATE: 2000-08-03
;; PRIOR APPLICATION NUMBER: 60/223,416
;; PRIOR FILING DATE: 2000-08-04
;; PRIOR APPLICATION NUMBER: 60/223,378
;; PRIOR FILING DATE: 2000-08-07
;; NUMBER OF SEQ ID NOS: 9597
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 321
;; LENGTH: 285
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-796-692-321

Query Match 21.5%; Score 285; DB 9; Length 285;

Best Local Similarity 100.0%; Pred. No. 1.3e-81; Indels 0; Gaps 0;

Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 682 CTGATATGTTGTTTACAGCTTTCTTCTCCCTTTGTCCTTACAGCACTAGTATTTCA 741
Db 285 CTGATATGTTGTTTACAGCTTTCTTCTCCCTTTGTCCTTACAGCACTAGTATTTCA 226
Qy 742 TGTGACACACCACTACAGCTCGTGAACCTGTGAGAACACAGCCGATTCACCTGACAG 801
Db 225 TGTGACACACCACTACAGCTCGTGAACCTGTGAGAACACAGCCGATTCACCTGACAG 166
Qy 802 ACTCTGAACCTTGACAGATGTTCTCAGATGTGTACATGCTTACCTGATTAACAGGCTT 861
Db 165 ACTCTGAACCTTGACAGATGTTCTCAGATGTGTACATGCTTACCTGATTAACAGGCTT 106
Qy 862 GCAAAAGCTGCTGCGGTAAACAGGCTTGAACAGCTGCTGCGGTAAACAGGCTTGA 921
Db 105 GCAAAAGCTGCTGCGGTAAACAGGCTTGAACAGCTGCTGCGGTAAACAGGCTTGA 46
Qy 922 AAAGCTGCTGCGGTAAACAGGCTTGAACAGCTGCTGCGGTAAACAGGCTTGA 966
Db 45 AAAGCTGCTGCGGTAAACAGGCTTGAACAGCTGCTGCGGTAAACAGGCTTGA 1

RESULT 11

US-09-796-692-468/c
;; Sequence 468, Application US/09796692
;; Publication No. US20020198362a1
;; GENERAL INFORMATION:
;; APPLICANT: Gaiger, Alexander
;; APPLICANT: Algate, Paul A.
;; APPLICANT: Mannion, Jane
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
;; FILE REFERENCE: 2077.001200
;; CURRENT APPLICATION NUMBER: US/09/796,692
;; PRIOR APPLICATION NUMBER: 2001-03-01
;; PRIOR FILING DATE: 2000-03-01
;; PRIOR APPLICATION NUMBER: 60/196,126
;; PRIOR FILING DATE: 2000-03-01
;; PRIOR APPLICATION NUMBER: 60/190,479
;; PRIOR FILING DATE: 2000-03-17
;; PRIOR APPLICATION NUMBER: 60/200,545
;; PRIOR FILING DATE: 2000-04-27
;; PRIOR APPLICATION NUMBER: 60/200,303
;; PRIOR FILING DATE: 2000-04-28
;; PRIOR APPLICATION NUMBER: 60/200,779
;; PRIOR FILING DATE: 2000-04-28
;; PRIOR APPLICATION NUMBER: 60/200,999
;; PRIOR FILING DATE: 2000-05-01
;; PRIOR APPLICATION NUMBER: 60/202,084


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/ PRIOR FILING DATE: 2000-08-03
/ PRIOR APPLICATION NUMBER: 60/223,416
/ PRIOR FILING DATE: 2000-08-04
/ PRIOR APPLICATION NUMBER: 60/223,378
/ PRIOR FILING DATE: 2000-08-07
/ NUMBER OF SEQ ID NOS: 9597
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO: 5832
/ LENGTH: 285
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-796-692-5832

Query Match      21.5%; Score 285; DB 9; Length 285;
Best Local Similarity 100.0%; Pred. No. 1,9e-81;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 682 CTGATGATGGTCTTTCAGCCTCTTCTGTCCCTTCTGCTCCCTCAGACAGCTAGTATTTC 741
DB 285 CTGATGATGGTCTTTCAGCCTCTTCTGTCCCTTCTGCTCCCTCAGACAGCTAGTATTTC 226
QY 742 TGTTCACACCCACTCAGCTCCGTGAACCTTGTGAACAACAGCCGATTCACTGACGAG 801
DB 225 TGTTCACACCCACTCAGCTCCGTGAACCTTGTGAACAACAGCCGATTCACTGACGAG 166
QY 802 ACCTCTGAACCCCTGGACAGTGTCTCAGATGGTCTACAGCCTGACATGTAACAGCGCT 861
DB 165 ACCTCTGAACCCCTGGACAGTGTCTCAGATGGTCTACAGCCTGACATGTAACAGCGCT 106
QY 862 GCAAAAGCTGCTGCGGTGAACACAGCCTGCAAAAGCTGCTGCGGTGAACACCGCTGC 921
DB 105 GCAAAAGCTGCTGCGGTGAACACAGCCTGCAAAAGCTGCTGCGGTGAACACCGCTGC 46
QY 922 AAAGCTGCTGCGGTGAACACAGCCTGCAAAAGCTGCTGCGGTGAACACCGCTGC 966
DB 45 AAAGCTGCTGCGGTGAACACAGCCTGCAAAAGCTGCTGCGGTGAACACCGCTGC 1

RESULT 14
US-09-796-692-6894/c
/ Sequence 6894, Application US/09796692
/ Publication No. US20020198362A1
/ GENERAL INFORMATION:
/ APPLICANT: Gaiger, Alexander
/ APPLICANT: Algate, Paul A.
/ APPLICANT: Mannion, Jane
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
/ FILE REFERENCE: 2077.001200
/ CURRENT APPLICATION NUMBER: US/09796,692
/ PRIOR FILING DATE: 2001-03-01
/ PRIOR APPLICATION NUMBER: 60/186,126
/ PRIOR FILING DATE: 2000-03-01
/ PRIOR APPLICATION NUMBER: 60/190,479
/ PRIOR FILING DATE: 2000-03-17
/ PRIOR APPLICATION NUMBER: 60/200,545
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: 60/200,303
/ PRIOR FILING DATE: 2000-04-28
/ PRIOR APPLICATION NUMBER: 60/200,779
/ PRIOR FILING DATE: 2000-04-28
/ PRIOR APPLICATION NUMBER: 60/200,999
/ PRIOR FILING DATE: 2000-05-01
/ PRIOR APPLICATION NUMBER: 60/202,084
/ PRIOR FILING DATE: 2000-05-04
/ PRIOR APPLICATION NUMBER: 60/206,201
/ PRIOR FILING DATE: 2000-05-22
/ PRIOR APPLICATION NUMBER: 60/218,950
/ PRIOR FILING DATE: 2000-07-14
/ PRIOR APPLICATION NUMBER: 60/222,903
/ PRIOR FILING DATE: 2000-08-03
/ PRIOR APPLICATION NUMBER: 60/223,416
/ PRIOR FILING DATE: 2000-08-04
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/ PRIOR APPLICATION NUMBER: 60/223,378
/ PRIOR FILING DATE: 2000-08-07
/ NUMBER OF SEQ ID NOS: 9597
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO: 6894
/ LENGTH: 285
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-796-692-6894

Query Match      21.5%; Score 285; DB 9; Length 285;
Best Local Similarity 100.0%; Pred. No. 1,9e-81;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 682 CTGATGATGGTCTTTCAGCCTCTTCTGTCCCTTCTGCTCCCTCAGACAGCTAGTATTTC 741
DB 285 CTGATGATGGTCTTTCAGCCTCTTCTGTCCCTTCTGCTCCCTCAGACAGCTAGTATTTC 226
QY 742 TGTTCACACCCACTCAGCTCCGTGAACCTTGTGAACAACAGCCGATTCACTGACGAG 801
DB 225 TGTTCACACCCACTCAGCTCCGTGAACCTTGTGAACAACAGCCGATTCACTGACGAG 166
QY 802 ACCTCTGAACCCCTGGACAGTGTCTCAGATGGTCTACAGCCTGACATGTAACAGCGCT 861
DB 165 ACCTCTGAACCCCTGGACAGTGTCTCAGATGGTCTACAGCCTGACATGTAACAGCGCT 106
QY 862 GCAAAAGCTGCTGCGGTGAACACAGCCTGCAAAAGCTGCTGCGGTGAACACCGCTGC 921
DB 105 GCAAAAGCTGCTGCGGTGAACACAGCCTGCAAAAGCTGCTGCGGTGAACACCGCTGC 46
QY 922 AAAGCTGCTGCGGTGAACACAGCCTGCAAAAGCTGCTGCGGTGAACACCGCTGC 966
DB 45 AAAGCTGCTGCGGTGAACACAGCCTGCAAAAGCTGCTGCGGTGAACACCGCTGC 1

RESULT 15
US-10-040-862-321/c
/ Sequence 321, Application US/10040862
/ Publication No. US20030078396A1
/ GENERAL INFORMATION:
/ APPLICANT: Gaiger, Alexander
/ APPLICANT: Algate, Paul A.
/ APPLICANT: Mannion, Jane
/ APPLICANT: Retter, Marc
/ APPLICANT: Corixa Corporation
/ TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
/ FILE REFERENCE: 014058-013520US
/ CURRENT APPLICATION NUMBER: US/10/040,862
/ PRIOR FILING DATE: 2001-11-06
/ PRIOR APPLICATION NUMBER: US 60/186,126
/ PRIOR FILING DATE: 2000-03-01
/ PRIOR APPLICATION NUMBER: US 60/190,479
/ PRIOR FILING DATE: 2000-03-17
/ PRIOR APPLICATION NUMBER: US 60/200,545
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 60/200,303
/ PRIOR FILING DATE: 2000-04-28
/ PRIOR APPLICATION NUMBER: US 60/200,779
/ PRIOR FILING DATE: 2000-04-28
/ PRIOR APPLICATION NUMBER: US 60/200,999
/ PRIOR FILING DATE: 2000-05-01
/ PRIOR APPLICATION NUMBER: US 60/202,084
/ PRIOR FILING DATE: 2000-05-04
/ PRIOR APPLICATION NUMBER: US 60/206,201
/ PRIOR FILING DATE: 2000-05-22
/ PRIOR APPLICATION NUMBER: US 60/218,950
/ PRIOR FILING DATE: 2000-07-14
/ PRIOR APPLICATION NUMBER: US 60/222,903
/ PRIOR FILING DATE: 2000-08-03
/ PRIOR APPLICATION NUMBER: US 60/223,416
/ PRIOR FILING DATE: 2000-08-04
/ PRIOR APPLICATION NUMBER: US 60/223,378
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; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq For Windows Version 3.0
; SEQ ID NO 321
; LENGTH: 285
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-040-862-321

Query Match 21.5%; Score 285; DB 15; Length 285;
Best Local Similarity 100.0%; Pred. No. 1.9e-81;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	682	CTGATGATGCTTTCAGCCTCTTCTGTGTCCTCTGTCCTCAAGACTAGTATTCA	741
DB	285	CTGATGATGCTTTCAGCCTCTTCTGTGTCCTCTGTCCTCAAGACTAGTATTCA	226
QY	742	TGTTGACACCCACTCAGCTCCGTGAACCTTGGAACAACAGCCGATTCACTGAGCAGG	801
DB	225	TGTTGACACCCACTCAGCTCCGTGAACCTTGGAACAACAGCCGATTCACTGAGCAGG	166
QY	802	ACCTCTGAAACCTGGAACAGTGTCTCAATGCTGACGCTGATGTAACACGCT	861
DB	165	ACCTCTGAAACCTGGAACAGTGTCTCAATGCTGACGCTGATGTAACACGCT	106
QY	862	GCAAAAGCTGCTGCGGTAAACAAGCGCTGCAAAAGCTGCGGTAAACAAGCGCTGC	921
DB	105	GCAAAAGCTGCTGCGGTAAACAAGCGCTGCAAAAGCTGCGGTAAACAAGCGCTGC	46
QY	922	AAAGCTGCTGCGGTAAACAAGCGCTGCAAAAGCTGCGGTAAACAAGCGCTGC	966
DB	45	AAAGCTGCTGCGGTAAACAAGCGCTGCAAAAGCTGCGGTAAACAAGCGCTGC	1

Search completed: June 17, 2004, 14:25:05
Job time : 618 secs